

FORM PTO-1390
(REV. 12-95)

U.S. DEPARTMENT OF COMMERCE, PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1761

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/623746

INTERNATIONAL APPLICATION NO.

PCT/DE99/00722

INTERNATIONAL FILING DATE

9 MARCH 1999

PRIORITY DATE CLAIMED

10 MARCH 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

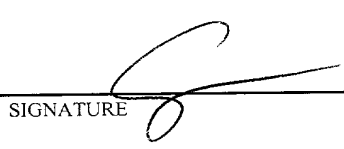


Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
- ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
- ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
- ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
 - ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: PAPER AND DISKETTE COPY OF SEQUENCE LISTING

U.S. APPLICATION NO (if known, see 37 CFR §1.5) 09/623746		INTERNATIONAL APPLICATION NO PCT/DE99/00722		ATTORNEY'S DOCKET NUMBER SCH 1761	
17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)): Search Report has been prepared by the EPO or JPO..... \$840.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$670.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$760.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$970.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$96.00 <div style="text-align: right;">ENTER APPROPRIATE BASIC FEE AMOUNT =</div>				CALCULATIONS PTO USE ONLY	
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	37 - 20 =	17	x \$ 18.00	\$306.00	
Independent claims	5 - 3 =	2	x \$ 78.00	\$156.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 260.00		
TOTAL OF ABOVE CALCULATIONS =				\$1,302.00	
Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
SUBTOTAL =				\$1,302.00	
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
TOTAL NATIONAL FEE =				\$1,302.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
TOTAL FEES ENCLOSED =				\$1,302.00	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,302.00</u> to cover the above fees is enclosed b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed					
NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: 8 SEPTEMBER 2000 AJZ:jmm				SIGNATURE  _____ Anthony J. Zelano NAME 27,969 REGISTRATION NUMBER	

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/00722
International Filing Date : 9 MARCH 1999
U.S. Serial No. : 09/623,746
Deposit Date U.S. Nat'l Phase : 8 SEPTEMBER 2000
Priority Date(s) Claimed : 10 MARCH 1998
Applicant(s) : SPECHT, Thomas, et al.
Title: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE



RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS
UNDER 35 U.S.C. § 371
IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

In response to the Notification of Missing Requirements mailed October 27, 2000, attached is a Declaration and Power of Attorney for Patent Application which has been executed by the inventors, as well as a copy of the Notification.

The Surcharge of \$130.00 for providing the Declaration later than 30 months from the original priority date is attached.

Applicants request that the time for responding to this action be extended one (1) month to December 27, 2000. A check for the statutory fee of \$110 is enclosed.

Also enclosed are ten (10) sheets of drawings, properly translated.

12/29/2000 UEDUVIJE 00000017 09623746

01 FC:154 130.00 OP
02 FC:115 110.00 OP

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE

International Application No. : PCT/DE99/00722
International Filing Date : 9 MARCH 1999
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Title: HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

Claim 5, line 1, delete "claims 1 to 4" and insert --Claim 3--;
Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;
Claim 7, line 2, delete "claims 1 to 6" and insert --Claim 3--;
line 4, delete "claims 1 to 6" and insert --Claim 3--;
Claim 8, line 1, delete "claims 1 to 7" and insert --Claim 3--;
Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;
Claim 10, lines 1 and 2, delete "claims 1 to 9" and insert --Claim 3--;
Claim 11, line 2, delete "one of claims 1 to 9" and insert --Claim 3--;
Claim 13, lines 1 and 2, delete "one of claims 11 and 12" and insert --Claim 11--;
Claim 14, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;
Claim 16, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;
Claim 18, line 1, delete "one of claims 16 or 17" and insert --Claim 16--;
Claim 19, line 2, delete "claims 16 to 18" and insert --Claim 16--;
Claim 26, line 1, after "partial sequences" insert --of Claim 23--;
Claim 27, line 1, after "acid sequences" insert --of Claim 2--;
Claim 28, line 1, after "acid sequences" insert --of Claim 2--;

Claim 29, line 1, after "partial sequences" insert --of Claim 23--;
Claim 30, line 1, after "partial sequences" insert --of Claim 23--;
Claim 31, line 2, after "partial sequence" insert --of Claim 23--;
Claim 32, line 1, delete "claims 1 to 10" and insert --Claim 3--;
Claim 33, line 1, delete "claims 1 to 10" and insert --Claim 3--;
Claim 34, line 3, after "sequences" insert --of Claim 2--;
Claim 37, line 1, delete "claims 1 to 7" and insert --Claim 3--.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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AJZ:jmm

Human Nucleic Acid Sequences from Prostate Tissue

The invention relates to human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal prostate tissue, which code for gene products or parts thereof and their use.

The invention furthermore relates to polypeptides that can be obtained via the sequences and their use.

One very common type of cancer is prostate cancer, for control of which new therapies are necessary. Previously used therapies that are based on a blocking of hormone effects are very often ineffective after a few years since the tumor becomes independent of the hormone, i.e., it continues to grow and forms metastases without the action of hormones.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database which consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue.

ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified which are important for tumor formation and proliferation (see Figure 1).

There is, however, the following problem: Since the EST sequences found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Therefore overlapping ESTs of the same gene were combined into longer sequences (see Figure 1, Figure 2a and Fig.

3). This lengthening and thus coverage of an essentially larger gene area in each of the respective bases are intended to largely avoid the above described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1 - 2b4.

Nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 which play a part as candidate genes in prostate cancer have now been found.

Nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 are of special interest.

The invention thus relates to nucleic acid sequences, which code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,
 - b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence which is complementary to the nucleic acid sequences named under a) or b).

The invention furthermore relates to a nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-

19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, which are expressed elevated in the normal prostate tissue.

The invention furthermore relates to nucleic acid sequences comprising part of the aforementioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 2500 bp, preferably a length of at least 150 to 2000 bp, especially a length from 400 to 1900 bp.

With the partial sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes and vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The obtainable genes are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments obtainable from use.

The nucleic acid sequences according to the invention can be moved into host cells with suitable vectors, in which as the

heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention furthermore relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

Furthermore, this invention relates to polypeptide partial sequences, so-called ORF (open-reading-frame) peptides according to the sequence protocols Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The invention furthermore relates to polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment and that are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The invention also relates to phage display proteins, which are directed against a polypeptide or a fragment, and which are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The polypeptides of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention can also be used as tools for finding active agents against prostate cancer; this is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 for expression of polypeptides, which can also be used as tools for finding active agents against prostate cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83,

90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer, or to produce a pharmaceutical agent for treatment of prostate cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice versions, obtainable from cDNAs of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in

order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as vehicles for gene transfer.

Meanings of technical terms and abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences which can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in different proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the alignment parameters

minimal initial match = minimal initial identity area
 maximum pads per read = maximum number of insertions
 maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the
 Incyte LifeSeq database.

Figure 2 shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

Figure 3 shows the in-silico subtraction of gene
 expression in different tissues

Figure 4a shows the determination of tissue-specific
 expression via electronic Northern

Figure 4b shows the electronic Northern

Figure 5 shows the isolation of genomic BAC and PAC
 clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence (see Figures 2a and 2b1-2b4).

The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the normal prostate tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (see Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated.

All sequences that occurred more than four times in one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2

Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E.W. and Lipman, D.J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T.L.; Schaeffer, A.A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D.J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W.R. and Lipman, D.J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in different EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blot.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 10 was found which occurs 4x more heavily in normal prostate tissue than in the corresponding tumor tissue.

The possible function of this gene region relates to human MVF-1.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 10

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0061	0.0052	1.1686	0.8557
Endocrine tissue	0.0055	0.0000	undef	0.0000
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0017	0.0088	0.1935	5.1673
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0050	0.0024	2.1069	0.4746
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0030	0.0068	0.4342	2.3033
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0017	0.0071	0.2321	4.3088
Breast hyperplasia	0.0145			
Small intestine	0.0000			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lung	0.0111
Kidney	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0040
Prostate	0.0128
Sensory organs	0.0000

2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 18 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 18

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0279	0.0026	10.9109	0.0917
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0116	0.0000	undef	0.0000
Brain	0.0042	0.0033	1.2902	0.7751
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0037	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0089	0.0000	undef	0.0000
Pancreas	0.0019	0.0055	0.3428	2.9168
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0033	0.0071	0.4642	2.1544
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0039
Lung	0.0000
Kidney	0.0000
Prostate	0.0124
Sensory organs	0.0000
	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0000
Nerves	0.0082
Prostate	0.0020
Sensory organs	0.0192
	0.0000

2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 24 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of an unknown gene yeast chromosome XVI.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 24

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0120	0.0131	0.9174	1.0901
Ovary	0.0091	0.0208	0.4382	2.2819
Endocrine tissue	0.0146	0.0191	0.7655	1.3064
Gastrointestinal	0.0233	0.0143	1.6285	0.6141
Brain	0.0034	0.0077	0.4423	2.2607
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0149	0.0847	0.1762	5.6754
Hepatic	0.0000	0.0518	0.0000	undef
Heart	0.0095	0.0275	0.3468	2.8832
Testicles	0.0061	0.0234	0.2612	3.8288
Lung	0.0100	0.0165	0.6020	1.6612
Stomach-esophagus	0.0097	0.0153	0.6300	1.5874
Muscle-skeleton	0.0051	0.0180	0.2855	3.5025
Kidney	0.0059	0.0000	undef	0.0000
Pancreas	0.0038	0.0221	0.1714	5.8337
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0214	0.0043	5.0338	0.1987
Uterus	0.0116	0.0142	0.8123	1.2311
Breast hyperplasia	0.0182			
Small intestine	0.0093			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			
FETUS				
	% freq.			
Development	0.0307			
Gastrointestinal	0.0123			
Brain	0.0125			
Hematopoietic	0.0118			
Heart-blood vessels	0.0082			
Lung	0.0000			
Kidney	0.0062			
Prostate	0.0000			
Sensory organs	0.0140			

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

2.1.4

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found which occurs 4x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of a gene of thaliana of Caenorhabditis elegans.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 30

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0152	0.0026	5.8431	0.1711
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0044	0.5806	1.7224
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0025	0.0024	1.0534	0.9493
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0000
Kidney	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0030
Sensory organs	0.0192
	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 43 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 43

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0120	0.0044	2.7521	0.3634
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0051	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lung	0.0012	0.0024	0.5267	1.8986
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0050	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0037
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0078
Lung	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 59 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 59

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0067	0.0022	3.0579	0.3270
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0091	0.0027	3.3489	0.2986
Gastrointestinal	0.0058	0.0000	undef	0.0000
Brain	0.0068	0.0088	0.7741	1.2918
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0183	0.0117	1.5671	0.6381
Lung	0.0062	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0154	0.0180	0.8565	1.1675
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0057	0.0166	0.3428	2.9168
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0333	0.0064	5.2203	0.1916
Uterus	0.0132	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0125			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0131			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lung	0.0148
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	
Hematopoietic	0.0244
Skin-muscle	0.0000
Testicles	0.0259
Lung	0.0000
Nerves	0.0000
Prostate	0.0010
Sensory organs	0.0064
	0.0000

In an analogous procedure, the following Northern blots were also found:

Electronic Northern Blot for Seq. ID No.: 2

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0418	0.0383	1.0911	0.9165
Breast	0.0267	0.0218	1.2232	0.8176
Ovary	0.0122	0.0052	2.3372	0.4279
Endocrine tissue	0.0055	0.0109	0.5023	1.9907
Gastrointestinal	0.0136	0.0048	2.8499	0.3509
Brain	0.0093	0.0142	0.6550	1.5267
Hematopoietic	0.0224	0.0000	undef	0.0000
Skin	0.0099	0.0847	0.1175	8.5131
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0061	0.0234	0.2612	3.8289
Lung	0.0137	0.0071	1.9313	0.5178
Stomach-esophagus	0.0193	0.0230	0.8399	1.1905
Muscle-skeleton	0.0103	0.0060	1.7130	0.5838
Kidney	0.0089	0.0000	undef	0.0000
Pancreas	0.0076	0.0110	0.6857	1.4584
Penis	0.0269	0.0000	undef	0.0000
Prostate	0.0143	0.0021	6.7118	0.1490
Uterus	0.0463	0.0356	1.2997	0.7694
Breast hyperplasia	0.0109			
Small intestine	0.0312			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0174			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0125
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lung	0.0370
Kidney	0.0124
Prostate	0.0748
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.1156
Ovary-uterus	0.0525
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lung	0.0082
Nerves	0.0151
Prostate	0.0385
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 3

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0093	0.0022	4.2811	0.2336
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0109	0.0027	4.0187	0.2488
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0068	0.0077	0.8847	1.1303
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0099	0.0065	1.5303	0.6535
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0030	0.0137	0.2171	4.6066
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
	0.0017			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0156
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 4

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0053	0.0022	2.4463	0.4088
Ovary	0.0030	0.0026	1.1686	0.8557
Endocrine tissue	0.0055	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0008	0.0055	0.1548	6.4591
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0089	0.0000	undef	0.0000
Pancreas	0.0038	0.0055	0.6857	1.4584
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0021	2.2373	0.4470
Uterus	0.0116	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0178			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

	0.0000
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0518
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 6

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0026	1.8185	0.5499
Breast	0.0053	0.0022	2.4463	0.4088
Ovary	0.0030	0.0026	1.1686	0.8557
Endocrine tissue	0.0055	0.0109	0.5023	1.9907
Gastrointestinal	0.0136	0.0048	2.8499	0.3509
Brain	0.0068	0.0066	1.0321	0.9689
Hematopoietic	0.0098	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0129	0.3826	2.6139
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0061	0.0117	0.5224	1.9144
Lungs	0.0100	0.0024	4.2137	0.2373
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0170	0.0055	3.0855	0.3241
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0017	0.0142	0.1160	8.6176
Breast hyperplasia	0.0036			
Small intestine	0.0062			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0096			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0079
Heart-blood vessels	0.0123
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0234
Lungs	0.0000
Nerves	0.0070
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 7

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0077	1.2123	0.8249
Bladder	0.0107	0.0131	0.8154	1.2263
Breast	0.0030	0.0078	0.3895	2.5671
Ovary	0.0146	0.0000	undef	0.0000
Endocrine tissue	0.0097	0.0143	0.6786	1.4737
Gastrointestinal	0.0170	0.0088	1.9353	0.5167
Brain	0.0098	0.0378	0.2587	3.8650
Hematopoietic	0.0298	0.0000	undef	0.0000
Skin	0.0000	0.0194	0.0000	undef
Hepatic	0.0159	0.0137	1.1561	0.8650
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0112	0.0142	0.7901	1.2657
Lungs	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0051	0.0060	0.8565	1.1675
Muscle-skeleton	0.0178	0.0068	2.6050	0.3839
Kidneys	0.0038	0.0387	0.0980	10.2089
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0095	0.0021	4.4745	0.2235
Prostate	0.0099	0.0000	undef	0.0000
Uterus	0.0109			
Breast hyperplasia	0.0125			
Small intestine	0.0119			
Prostatic hyperplasia	0.0356			
Seminal vesicles	0.0000			
Sensory organs	0.0096			
White blood cells				

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0188
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0148
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0057
Skin-muscle	0.0162
Testicles	0.0078
Lungs	0.0492
Nerves	0.0161
Prostate	0.0192
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 8

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0109	1.1008	0.9084
Breast	0.0061	0.0052	1.1686	0.8557
Ovary	0.0146	0.0136	1.0716	0.9331
Endocrine tissue	0.0155	0.0143	1.0857	0.9211
Gastrointestinal	0.0136	0.0142	0.9527	1.0496
Brain	0.0042	0.0000	undef	0.0000
Hematopoietic	0.0149	0.0000	undef	0.0000
Skin	0.0050	0.0065	0.7651	1.3069
Hepatic	0.0170	0.0000	undef	0.0000
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0112	0.0095	1.1851	0.8438
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0060	0.8565	1.1675
Muscle-skeleton	0.0119	0.0068	1.7366	0.5758
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0143	0.0064	2.2373	0.4470
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0030			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0113			
White blood cells				

FETUS
% freq.

	0.0000
Development	0.0123
Gastrointestinal	0.0063
Brain	0.0000
Hematopoietic	0.0164
Heart-blood vessels	0.0037
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0156
Lungs	0.0082
Nerves	0.0191
Prostate	0.0064
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 9

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0026	9.0924 0.1100
Bladder	0.0187	0.0087	2.1405 0.4672
Breast	0.0122	0.0156	0.7791 1.2836
Ovary	0.0219	0.0136	1.6075 0.6221
Endocrine tissue	0.0116	0.0190	0.6107 1.6375
Gastrointestinal	0.0119	0.0142	0.8337 1.1995
Brain	0.0126	0.0000	undef 0.0000
Hematopoietic	0.0199	0.0000	undef 0.0000
Skin	0.0099	0.0000	undef 0.0000
Hepatic	0.0159	0.0137	1.1561 0.8650
Heart	0.0122	0.0351	0.3482 2.8716
Testicles	0.0187	0.0378	0.4938 2.0251
Lungs	0.0097	0.0307	0.3150 3.1748
Stomach-esophagus	0.0103	0.0120	0.8565 1.1675
Muscle-skeleton	0.0238	0.0000	undef 0.0000
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0180	0.0267	0.6739 1.4840
Penis	0.0214	0.0085	2.5169 0.3973
Prostate	0.0132	0.0285	0.4642 2.1544
Uterus	0.0291		
Breast hyperplasia	0.0156		
Small intestine	0.0268		
Prostatic hyperplasia	0.0356		
Seminal vesicles	0.0235		
Sensory organs	0.0131		
White blood cells			

FETUS
% freq.

	0.0307
Development	0.0247
Gastrointestinal	0.0063
Brain	0.0236
Hematopoietic	0.0286
Heart-blood vessels	0.0111
Lungs	0.0371
Kidneys	0.0997
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0312
Lungs	0.0082
Nerves	0.0050
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 12

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0027	0.0044	0.6116 1.6351
Ovary	0.0000	0.0156	0.0000 undef
Endocrine tissue	0.0018	0.0027	0.6698 1.4930
Gastrointestinal	0.0078	0.0000	undef 0.0000
Brain	0.0034	0.0011	3.0964 0.3230
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0112	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0060	0.5710 1.7513
Kidneys	0.0089	0.0068	1.3025 0.7678
Pancreas	0.0076	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0156		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0052		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0156
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 13

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0128	0.0000 undef
Breast	0.0120	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0036	0.0000	undef 0.0000
Gastrointestinal	0.0039	0.0000	undef 0.0000
Brain	0.0017	0.0066	0.2580 3.8754
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0074	0.0000	undef 0.0000
Testicles	0.0000	0.0117	0.0000 undef
Lungs	0.0087	0.0071	1.2290 0.8137
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0060	1.4275 0.7005
Kidneys	0.0000	0.0137	0.0000 undef
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0150	0.0000	undef 0.0000
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0066	0.0071	0.9283 1.0772
Breast hyperplasia	0.0218		
Small intestine	0.0062		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0089		
Sensory organs	0.0353		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 14

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0051	0.9092	1.0998
Breast	0.0027	0.0000	undef	0.0000
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1541	6.4872
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0012	0.0024	0.5267	1.8986
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0167	0.0000	undef	0.0000
Uterus	0.0017	0.0071	0.2321	4.3088
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0078
Nerves	0.0000
Prostate	0.0020
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 16

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0120	0.0022	5.5042	0.1817
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0049	0.4071	2.4562
Brain	0.0085	0.0219	0.3871	2.5836
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0259	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0037	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0223	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0192	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

	0.0000
Development	0.0062
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0041
Heart-blood vessels	0.0037
Lungs	0.0124
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 17

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0053	0.0065	0.8154	1.2263
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0091	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0048	0.4071	2.4562
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0042	0.0378	0.1109	9.0183
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0112	0.0071	1.5801	0.6329
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0060	1.4275	0.7005
Kidneys	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0057	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0050	0.0071	0.6963	1.4363
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0089			
Sensory organs	0.0118			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0164
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0387

Electronic Northern Blot for SEQ. ID. NO: 19

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0128	0.7274	1.3748
Breast	0.0080	0.0065	1.2232	0.8176
Breast	0.0091	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0042	0.0044	0.9676	1.0335
Brain	0.0070	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0032	0.0137	0.2312	4.3248
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0118	0.3160	3.1643
Lungs	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidneys	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0119	0.0064	1.8644	0.5364
Prostate	0.0099	0.0000	undef	0.0000
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0089			
Prostatic hyperplasia	0.0178			
Seminal vesicles	0.0000			
Sensory organs	0.0044			
White blood cells				

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Brain	0.0157
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0192
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 21

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0128	0.3637	2.7495
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0061	0.0104	0.5843	1.7114
Endocrine tissue	0.0128	0.0136	0.9377	1.0664
Gastrointestinal	0.0078	0.0143	0.5428	1.8422
Brain	0.0102	0.0131	0.7741	1.2918
Hematopoietic	0.0042	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0165	0.1505	6.6450
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9993	1.0007
Kidneys	0.0178	0.0068	2.6050	0.3839
Pancreas	0.0076	0.0110	0.6857	1.4584
Penis	0.0090	0.0267	0.3369	2.9680
Prostate	0.0167	0.0064	2.6101	0.3831
Uterus	0.0066	0.0214	0.3094	3.2316
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0208			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0247
Brain	0.0188
Hematopoietic	0.0079
Heart-blood vessels	0.0245
Lungs	0.0037
Kidneys	0.0247
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0259
Testicles	0.0000
Lungs	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 23

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0030	0.0078	0.3895	2.5671
Endocrine tissue	0.0036	0.0054	0.6698	1.4930
Gastrointestinal	0.0039	0.0048	0.8143	1.2281
Brain	0.0025	0.0033	0.7741	1.2918
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0047	0.5267	1.8986
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0060	0.2855	3.5025
Kidneys	0.0089	0.0068	1.3025	0.7678
Pancreas	0.0095	0.0055	1.7142	0.5834
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0149			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0026	0.0000	undef
Bladder	0.0027	0.0044	0.6116	1.6351
Breast	0.0061	0.0052	1.1686	0.8557
Ovary	0.0109	0.0027	4.0187	0.2488
Endocrine tissue	0.0019	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0011	6.1928	0.1615
Brain	0.0028	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0129	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0122	0.0000	undef	0.0000
Testicles	0.0012	0.0071	0.1756	5.6957
Lungs	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0017	0.0060	0.2855	3.5025
Muscle-skeleton	0.0030	0.0068	0.4342	2.3033
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0119	0.0000	undef	0.0000
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0000			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0078
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 27

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0027	0.0022	1.2232	0.8176
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 28

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0000	undef	0.000
Ovary	0.0030	0.0052	0.5843	1.7114
Endocrine tissue	0.0036	0.0027	1.3396	0.7465
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0183	0.0000	undef	0.0000
Lungs	0.0050	0.0024	2.1069	0.4746
Stomach-esophagus	0.0097	0.0077	1.2599	0.7937
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0019	0.0110	0.1714	5.8337
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0043	2.7966	0.3576
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 29

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0055	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0093	0.0022	4.2576	0.2349
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0065	0.7651	1.3069
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0066	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0000
Nerves	0.0141
Prostate	0.0256
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 31

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0048	0.4071	2.4562
Brain	0.0000	0.0022	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 32

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0027	0.0022	1.2232	0.8176
Ovary	0.0091	0.0078	1.1686	0.8557
Endocrine tissue	0.0055	0.0136	0.4019	2.4884
Gastrointestinal	0.0019	0.0095	0.2036	4.9124
Brain	0.0076	0.0044	1.7417	0.5741
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0012	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5076
Kidneys	0.0030	0.0068	0.4342	2.3033
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0017	0.0142	0.1160	8.6176
Breast hyperplasia	0.0109			
Small intestine	0.0062			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

	0.0000
Development	0.0154
Gastrointestinal	0.0125
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0097
Testicles	0.0468
Lungs	0.0082
Nerves	0.0060
Prostate	0.0192
Sensory organs	0.0232

Electronic Northern Blot for SEQ. ID. NO: 33

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0013	0.0022	0.6116 1.6351
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0055	0.0000	undef 0.0000
Gastrointestinal	0.0019	0.0000	undef 0.0000
Brain	0.0042	0.0077	0.5529 1.8085
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0117	0.0000 undef
Lungs	0.0025	0.0047	0.5267 1.8986
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0062		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0017		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 35

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0093	0.0065	1.4270 0.7008
Breast	0.0091	0.0130	0.7012 1.4262
Ovary	0.0055	0.0027	2.0093 0.4977
Endocrine tissue	0.0039	0.0190	0.2036 4.9124
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0112	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0053	0.0137	0.3854 2.5949
Heart	0.0000	0.0000	undef undef
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0089	0.0137	0.6512 1.5355
Kidneys	0.0057	0.0000	undef 0.0000
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0095	0.0021	4.4745 0.2235
Prostate	0.0033	0.0000	undef 0.0000
Uterus	0.0000		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0009		
White blood cells			

FETUS
% freq.

	0.0000
Development	0.0154
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0082
Heart-blood vessels	0.0074
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0297
Ovary-uterus	0.0245
Endocrine tissue	0.0082
Fetal	0.0000
Gastrointestinal	0.0057
Hematopoietic	0.0032
Skin-muscle	0.0156
Testicles	0.0000
Lungs	0.0080
Nerves	0.0064
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 36

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0077	0.6062	1.6497
Breast	0.0013	0.0153	0.0874	11.4458
Ovary	0.0091	0.0026	3.5059	0.2852
Endocrine tissue	0.0036	0.0054	0.6698	1.4930
Gastrointestinal	0.0174	0.0048	3.6642	0.2729
Brain	0.0034	0.0000	undef	0.0000
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0249	0.0000	undef	0.0000
Hepatic	0.0248	0.0000	undef	0.0000
Heart	0.0032	0.0137	0.2312	4.3248
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0261	0.0095	2.7652	0.3616
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0297	0.0000	undef	0.0000
Pancreas	0.0095	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0143	0.0064	2.2373	0.4470
Uterus	0.0050	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0031			
Prostatic hyperplasia	0.0149			
Seminal vesicles	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0246
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 37

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0050	0.0356	0.1393	7.1813
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 39

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0325	0.0332	0.9792 1.0213
Breast	0.0293	0.0196	1.4950 0.6689
Ovary	0.0000	0.0104	0.0000 undef
Endocrine tissue	0.0091	0.0000	undef 0.0000
Gastrointestinal	0.0252	0.0000	undef 0.0000
Brain	0.0085	0.0131	0.6451 1.5502
Hematopoietic	0.0098	0.0000	undef 0.0000
Skin	0.0249	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0636	0.1649	0.3854 2.5949
Testicles	0.0183	0.0000	undef 0.0000
Lungs	0.0212	0.0165	1.2792 0.7818
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0137	0.0060	2.2841 0.4378
Kidneys	0.0208	0.0137	1.5196 0.6581
Pancreas	0.0284	0.0166	1.7142 0.5834
Penis	0.0000	0.0533	0.0000 undef
Prostate	0.0048	0.0106	0.4475 2.2349
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0218		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0000		
Sensory organs	0.0588		
White blood cells	0.1045		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0118
Heart-blood vessels	0.0041
Lungs	0.0148
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0114
Endocrine tissue	0.1224
Fetal	0.0122
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0164
Nerves	0.0040
Prostate	0.0385
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 41

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0022	0.0000	undef
Breast	0.0061	0.0026	2.3372	0.4279
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 42

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0160	0.0044	3.6695	0.2725
Ovary	0.0030	0.0026	1.1686	0.8557
Endocrine tissue	0.0109	0.0082	1.3396	0.7465
Gastrointestinal	0.0078	0.0000	undef	0.0000
Brain	0.0042	0.0055	0.7741	1.2918
Hematopoietic	0.0070	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0037	0.0024	1.5801	0.6329
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0057	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0167	0.0000	undef	0.0000
Uterus	0.0066	0.0000	undef	0.0000
Breast hyperplasia	0.0109			
Small intestine	0.0031			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 44

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0372	0.0230	1.6164	0.6186
Breast	0.0067	0.0000	undef	0.0000
Ovary	0.0122	0.0130	0.9349	1.0696
Endocrine tissue	0.0128	0.0300	0.4262	2.3462
Gastrointestinal	0.0271	0.0333	0.8143	1.2281
Brain	0.0059	0.0471	0.1260	7.9354
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0099	0.0000	undef	0.0000
Hepatic	0.0050	0.0259	0.1913	5.2277
Heart	0.0201	0.0137	1.4644	0.6829
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0274	0.0189	1.4485	0.6904
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidneys	0.0089	0.0137	0.6512	1.5355
Pancreas	0.0076	0.0166	0.4571	2.1876
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0333	0.0106	3.1322	0.3193
Uterus	0.0215	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0280			
Prostatic hyperplasia	0.0357			
Seminal vesicles	0.0890			
Sensory organs	0.0235			
White blood cells	0.0052			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0222
Kidneys	0.0309
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0227
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0000
Lungs	0.0082
Nerves	0.0050
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 46

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0040	0.0131	0.3058 3.2702
Ovary	0.0122	0.0234	0.5194 1.9254
Endocrine tissue	0.0036	0.0109	0.3349 2.9861
Gastrointestinal	0.0116	0.0095	1.2214 0.8187
Brain	0.0051	0.0164	0.3096 3.2295
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0085	0.0137	0.6166 1.6218
Testicles	0.0061	0.0117	0.5224 1.9144
Lungs	0.0075	0.0095	0.7901 1.2657
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidneys	0.0030	0.0068	0.4342 2.3033
Pancreas	0.0076	0.0055	1.3713 0.7292
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0119	0.0043	2.7966 0.3576
Uterus	0.0083	0.0071	1.1604 0.8618
Breast hyperplasia	0.0036		
Small intestine	0.0093		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0118		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0154
Brain	0.0125
Hematopoietic	0.0157
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0117
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0164
Nerves	0.0110
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 47

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0077	1.2123	0.8249
Breast	0.0093	0.0283	0.3293	3.0366
Ovary	0.0182	0.0052	3.5059	0.2852
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0504	0.0000	undef	0.0000
Brain	0.0000	0.0033	0.0000	undef
Hematopoietic	0.0042	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0495	0.0065	7.6515	0.1307
Heart	0.0074	0.0137	0.5395	1.8535
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9985	0.5004
Kidneys	0.0238	0.0000	undef	0.0000
Pancreas	0.0511	0.0276	1.8513	0.5402
Penis	0.0000	0.0000	undef	undef
Prostate	0.0333	0.0149	2.2373	0.4470
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0109			
Small intestine	0.1028			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0183			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0462
Brain	0.0000
Hematopoietic	0.0197
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 51

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0465	0.0741	0.6271 1.5947
Breast	0.0386	0.0501	0.7711 1.2968
Ovary	0.0334	0.0546	0.6121 1.6336
Endocrine tissue	0.0310	0.0300	1.0351 0.9661
Gastrointestinal	0.0252	0.0190	1.3232 0.7558
Brain	0.0458	0.0701	0.6532 1.5310
Hematopoietic	0.0112	0.1135	0.0986 10.1456
Skin	0.0448	0.0000	undef 0.0000
Hepatic	0.0347	0.0000	undef 0.0000
Heart	0.1123	0.1375	0.8170 1.2240
Testicles	0.0366	0.0468	0.7835 1.2763
Lungs	0.0535	0.0449	1.1920 0.8389
Stomach-esophagus	0.0193	0.0153	1.2599 0.7937
Muscle-skeleton	0.0685	0.1860	0.3684 2.7145
Kidneys	0.0119	0.0890	0.1336 7.4857
Pancreas	0.0151	0.0828	0.1828 5.4691
Penis	0.1018	0.0533	1.9092 0.5238
Prostate	0.0167	0.0064	2.6101 0.3831
Uterus	0.0545	0.2634	0.2070 4.8311
Breast hyperplasia	0.0981		
Small intestine	0.0312		
Prostatic hyperplasia	0.0386		
Seminal vesicles	0.0178		
Sensory organs	0.0235		
White blood cells	0.0009		

FETUS
% freq.

Development	0.1383
Gastrointestinal	0.0924
Brain	0.0063
Hematopoietic	0.0393
Heart-blood vessels	0.0654
Lungs	0.0592
Kidneys	0.0309
Prostate	0.2992
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0171
Prostate	0.0000
Sensory organs	0.0387

Electronic Northern Blot for SEQ. ID. NO: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0022	0.6116	1.6351
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0036	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0008	0.0099	0.0860	11.6263
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0083	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 53

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0044	0.0000	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0055	0.0027	2.0093	0.4977
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0071	0.0021	3.3559	0.2980
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 54

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0200	0.0044	4.5868 0.2180
Ovary	0.0152	0.0104	1.4608 0.6846
Endocrine tissue	0.0091	0.0054	1.6745 0.5972
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0110	0.0033	3.3545 0.2981
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0198	0.0000	undef 0.0000
Heart	0.0064	0.0000	undef 0.0000
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0062	0.0071	0.8779 1.1391
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0051	0.0240	0.2141 4.6701
Kidneys	0.0178	0.0000	undef 0.0000
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0119	0.0043	2.7966 0.3576
Uterus	0.0050	0.0214	0.2321 4.3088
Breast hyperplasia	0.0000		
Small intestine	0.0062		
Prostatic hyperplasia	0.0208		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0540		

FETUS
% freq.

	0.0000
Development	0.0123
Gastrointestinal	0.0250
Brain	0.0275
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0558

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0064
Sensory organs	0.0310

Electronic Northern Blot for SEQ. ID. NO: 55

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6497
Breast	0.0053	0.0065	0.8154 1.2263
Ovary	0.0000	0.0052	0.0000 undef
Endocrine tissue	0.0055	0.0054	1.0047 0.9954
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0042	0.0033	1.2902 0.7751
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0050	0.0129	0.3826 2.6139
Heart	0.0074	0.0000	undef 0.0000
Testicles	0.0061	0.0234	0.2612 3.8288
Lungs	0.0100	0.0095	1.0534 0.9493
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0089	0.0137	0.6512 1.5355
Pancreas	0.0057	0.0000	undef 0.0000
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0066	0.0071	0.9283 1.0772
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0089		
Sensory organs	0.0118		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 58

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0080	0.0022	3.6695	0.2725
Ovary	0.0061	0.0078	0.7791	1.2836
Endocrine tissue	0.0018	0.0109	0.1674	5.9721
Gastrointestinal	0.0078	0.0143	0.5428	1.8422
Brain	0.0034	0.0033	1.0321	0.9689
Hematopoietic	0.0084	0.0000	undef	0.0000
Skin	0.0895	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0137	0.2312	4.3248
Testicles	0.0183	0.0000	undef	0.0000
Lungs	0.0037	0.0142	0.2634	3.7971
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0000	0.0068	0.0000	undef
Pancreas	0.0038	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0071	0.0021	3.3559	0.2980
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0182			
Small intestine	0.0031			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0000
Brain	0.0157
Hematopoietic	0.0082
Heart-blood vessels	0.0148
Lungs	0.0124
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0156
Lungs	0.0082
Nerves	0.0080
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 60

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0068	0.0033	2.0643	0.4844
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 61

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0128	0.0000 undef
Breast	0.0000	0.0022	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0018	0.0109	0.1674 5.9721
Gastrointestinal	0.0078	0.0000	undef 0.0000
Brain	0.0034	0.0033	1.0321 0.9689
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0032	0.0000	undef 0.0000
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0025	0.0071	0.3511 2.8478
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0071	0.0021	3.3559 0.2980
Prostate	0.0033	0.0000	undef 0.0000
Uterus	0.0000		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0164
Nerves	0.0050
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 62

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0133	0.0022	6.1158 0.1635
Ovary	0.0061	0.0052	1.1686 0.8557
Endocrine tissue	0.0000	0.0245	0.0000 undef
Gastrointestinal	0.0078	0.0190	0.4071 2.4562
Brain	0.0119	0.0022	5.4187 0.1845
Hematopoietic	0.0070	0.0757	0.0924 10.8219
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0000	undef 0.0000
Heart	0.0074	0.0275	0.2698 3.7070
Testicles	0.0000	0.0234	0.0000 undef
Lungs	0.0050	0.0118	0.4214 2.3732
Stomach-esophagus	0.0097	0.0153	0.6300 1.5874
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0119	0.0205	0.5789 1.7275
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0191	0.0043	4.4745 0.2235
Uterus	0.0066	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0031		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0070		

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0309
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0161
Prostate	0.0128
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 63

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0186	0.0844	0.2204 4.5368
Breast	0.0560	0.0370	1.5110 0.6618
Ovary	0.0395	0.0260	1.5192 0.6582
Endocrine tissue	0.0128	0.0245	0.5209 1.9196
Gastrointestinal	0.0775	0.0857	0.9047 1.1053
Brain	0.0254	0.0350	0.7257 1.3779
Hematopoietic	0.0364	0.0378	0.9610 1.0406
Skin	0.2188	0.0000	undef 0.0000
Hepatic	0.0198	0.0582	0.3401 2.9406
Heart	0.1112	0.1787	0.6225 1.6064
Testicles	0.0183	0.0117	1.5671 0.6381
Lungs	0.1133	0.0804	1.4097 0.7094
Stomach-esophagus	0.0676	0.0307	2.2049 0.4535
Muscle-skeleton	0.1696	0.0300	5.6530 0.1769
Kidneys	0.0684	0.0753	0.9078 1.1016
Pancreas	0.0151	0.0607	0.2493 4.0107
Penis	0.0749	0.1066	0.7019 1.4246
Prostate	0.0715	0.0106	6.7118 0.1490
Uterus	0.0611	0.0214	2.8624 0.3494
Breast hyperplasia	0.0254		
Small intestine	0.0997		
Prostatic hyperplasia	0.0386		
Seminal vesicles	0.0445		
Sensory organs	0.0941		
White blood cells	0.0670		

FETUS
% freq.

Development	0.0615
Gastrointestinal	0.0154
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0338
Gastrointestinal	0.1098
Hematopoietic	0.0114
Skin-muscle	0.0421
Testicles	0.0312
Lungs	0.2786
Nerves	0.0080
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 64

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6497
Breast	0.0160	0.0174	0.9174 1.0901
Ovary	0.0091	0.0182	0.5008 1.9967
Endocrine tissue	0.0201	0.0109	1.8419 0.5429
Gastrointestinal	0.0194	0.0333	0.5816 1.7193
Brain	0.0076	0.0219	0.3483 2.8707
Hematopoietic	0.0182	0.0378	0.4805 2.0811
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0323	0.3061 3.2673
Heart	0.0148	0.0275	0.5395 1.8535
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0174	0.0118	1.4748 0.6781
Stomach-esophagus	0.0290	0.0307	0.9449 1.0583
Muscle-skeleton	0.0154	0.0120	1.2848 0.7783
Kidneys	0.0416	0.0068	6.0782 0.1645
Pancreas	0.0170	0.0110	1.5428 0.6482
Penis	0.0120	0.0267	0.4492 2.2260
Prostate	0.0191	0.0085	2.2373 0.4470
Uterus	0.0149	0.0142	1.0444 0.9575
Breast hyperplasia	0.0182		
Small intestine	0.0187		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0178		
Sensory organs	0.0353		
White blood cells	0.0183		

FETUS
% freq.

	0.0307
Development	0.0062
Gastrointestinal	0.0000
Brain	0.0393
Hematopoietic	0.0000
Heart-blood vessels	0.0074
Lungs	0.0124
Kidneys	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Ovary-uterus	0.0571
Endocrine tissue	0.0245
Fetal	0.0175
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0082
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0310

Electronic Northern for Seq. ID: 217

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0039	0.0094	0.4149 2.4102
Breast	0.0053	0.0028	1.8786 0.5323
Large intestine	0.0153	0.0028	5.3823 0.1858
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0032	0.0114	0.2826 3.5381
Brain	0.0072	0.0060	1.2090 0.8271
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0046	0.0127	0.3662 2.7307
Heart	0.0071	0.0137	0.5169 1.9348
Testicles	0.0080	0.0059	1.3570 0.7369
Lung	0.0107	0.0037	2.8941 0.3455
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0086	0.0000	undef 0.0000
Kidney	0.0045	0.0048	0.9284 1.0771
Pancreas	0.0116	0.0055	2.0940 0.4776
Prostate	0.0038	0.0013	2.8940 0.3455
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0031	0.0092	0.3368 2.9694
White blood cells	0.0089	0.0000	undef 0.0000
Hematopoietic	0.0067		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0125
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0203
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 218

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0078	0.0117	0.6638 1.5064
Breast	0.0114	0.0169	0.6784 1.4741
Large intestine	0.0115	0.0085	1.3456 0.7432
Small intestine	0.0110	0.0107	1.0306 0.9703
Ovary	0.0059	0.0072	0.8295 1.2055
Endocrine tissue	0.0144	0.0038	3.8156 0.2621
Brain	0.0193	0.0110	1.7586 0.5686
Skin	0.0220	0.0000	undef 0.0000
Hepatic	0.0000	0.0190	0.0000 undef
Heart	0.0173	0.0137	1.2552 0.7967
Testicles	0.0080	0.0059	1.3570 0.7369
Lung	0.0165	0.0111	1.4909 0.6707
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0179	0.0048	3.7136 0.2693
Pancreas	0.0033	0.0442	0.0748 13.3714
Prostate	0.0085	0.0039	2.1705 0.4607
T lymphoma	0.0101	0.0075	1.3525 0.7394
Uterus	0.0093	0.0138	0.6735 1.4847
White blood cells	0.0096	0.0304	0.3156 3.1685
Hematopoietic	0.0094		
Penis	0.0134		
Seminal vesicle	0.0352		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0513
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0586
Lungs_t	0.0000
Nerves	0.0161
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0182
White blood cells	0.0077
	0.0000

Electronic Northern for Seq. ID: 219

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0075	0.0000	undef	0.0000
Bladder	0.0156	0.0047	3.3190	0.3013
Breast	0.0185	0.0211	0.8767	1.1406
Large intestine	0.0307	0.0199	1.5378	0.6503
Small intestine	0.0082	0.0213	0.3865	2.5875
Ovary	0.0059	0.0334	0.1778	5.6255
Endocrine tissue	0.0305	0.0266	1.1468	0.8720
Brain	0.0393	0.0189	2.0767	0.4815
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0000	0.0127	0.0000	undef
Heart	0.0447	0.0000	undef	0.0000
Testicles	0.0161	0.0118	1.3571	0.7369
Lung	0.0282	0.0240	1.1739	0.8519
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0154	0.0074	2.0875	0.4790
Kidney	0.0269	0.0193	1.3927	0.7180
Pancreas	0.0066	0.0000	undef	0.0000
Prostate	0.0179	0.0065	2.7494	0.3637
T lymphoma	0.0177	0.0672	0.2630	3.8026
Uterus	0.0118	0.0046	2.5703	0.3891
White blood cells	0.0226	0.0000	undef	0.0000
Hematopoietic	0.0147			
Penis	0.0188			
Seminal vesicle	0.0281			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0145
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0292
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0311
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0061
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 220

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0088	0.0070	1.2524	0.7985
Large intestine	0.0153	0.0085	1.7941	0.5574
Small intestine	0.0192	0.0213	0.9018	1.1089
Ovary	0.0059	0.0262	0.2262	4.4200
Endocrine tissue	0.0337	0.0142	2.3766	0.4208
Brain	0.0156	0.0070	2.2381	0.4468
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0093	0.0063	1.4649	0.6826
Heart	0.0183	0.0000	undef	0.0000
Testicles	0.0161	0.0059	2.7142	0.3684
Lung	0.0185	0.0111	1.6663	0.6001
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0157	0.0048	3.2497	0.3077
Pancreas	0.0099	0.0055	1.7949	0.5571
Prostate	0.0160	0.0065	2.4600	0.4065
T lymphoma	0.0152	0.0299	0.5072	1.9717
Uterus	0.0089	0.0046	1.9277	0.5188
White blood cells	0.0164	0.0304	0.5410	1.8483
Hematopoietic	0.0040			
Penis	0.0080			
Seminal vesicle	0.0141			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0178
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 221

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0000	undef	0.0000
Bladder	0.0078	0.0047	1.6595	0.6026
Breast	0.0079	0.0056	1.4090	0.7097
Large intestine	0.0057	0.0085	0.6728	1.4864
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0030	0.0143	0.2074	4.8219
Endocrine tissue	0.0112	0.0106	1.0563	0.9467
Brain	0.0052	0.0040	1.3056	0.7659
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0132	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0117	0.0129	0.9021	1.1085
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0086	0.0074	1.1597	0.8623
Kidney	0.0179	0.0048	3.7139	0.2693
Pancreas	0.0083	0.0000	undef	0.0000
Prostate	0.0113	0.0065	1.7364	0.5759
T lymphoma	0.0000	0.0149	0.0000	undef
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0075	0.0304	0.2480	4.0326
Hematopoietic	0.0067			
Penis	0.0080			
Seminal vesicle	0.0141			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0050
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0121
Sensory organs	0.0774
White blood cells	0.0000

Electronic Northern for Seq. ID: 222

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0351	0.0047	7.4677	0.1339
Breast	0.0070	0.0014	5.0097	0.1996
Large intestine	0.0115	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0016	0.0035	0.4527	2.2091
Brain	0.0017	0.0060	0.2901	3.4467
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0020	0.0137	0.1477	6.7715
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0039	0.0018	2.1049	0.4751
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0112	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2992	3.3427
Prostate	0.0075	0.0026	2.8941	0.3455
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0059	0.0046	1.2851	0.7781
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 223

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0000	undef 0.0000
Bladder	0.0273	0.0117	2.3233 0.4304
Breast	0.0150	0.0098	1.5208 0.6576
Large intestine	0.0077	0.0028	2.6911 0.3716
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0089	0.0024	3.7330 0.2679
Endocrine tissue	0.0016	0.0053	0.3018 3.3136
Brain	0.0069	0.0100	0.6963 1.4361
Hepatic	0.0037	0.0000	undef 0.0000
Heart	0.0000	0.0190	0.0000 undef
Testicles	0.0081	0.0137	0.5907 1.6929
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0068	0.0111	0.6139 1.6289
Muscle-skeleton	0.0072	0.0128	0.5668 1.7644
Kidney	0.0086	0.0037	2.3194 0.4311
Pancreas	0.0112	0.0000	undef 0.0000
Prostate	0.0050	0.0055	0.8975 1.1142
T lymphoma	0.0141	0.0169	0.8348 1.1978
Uterus	0.0202	0.0075	2.7049 0.3697
White blood cells	0.0177	0.0000	undef 0.0000
Hematopoietic	0.0096	0.0000	undef 0.0000
Penis	0.0187		
Seminal vesicle	0.0080		
Sensory organs	0.0281		
	0.0000		
	FETUS % freq.		
Development	0.0000		
Gastrointestinal	0.0056		
Brain	0.0000		
Hematopoietic	0.0157		
Skin	0.0000		
Hepatic	0.0000		
Heart-blood vessels	0.0071		
Lung	0.0145		
Adrenal gland	0.0000		
Kidney	0.0062		
Placenta	0.0000		
Prostate	0.0000		
Sensory organs	0.0000		

STANDARDIZED/SUBTRACTED LIBRARIES

	0.0068 % frequency
Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0121
Sensory organs	0.0155
White blood cells	0.0000

Electronic Northern for Seq. ID: 224

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0018	0.0112	0.1566	6.3876
Large intestine	0.0057	0.0057	1.0092	0.9909
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0059	0.0143	0.4148	2.4109
Endocrine tissue	0.0032	0.0053	0.6036	1.6568
Brain	0.0029	0.0060	0.4835	2.0680
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0093	0.0000	undef	0.0000
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0039	0.0037	1.0524	0.9502
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0112	0.0048	2.3212	0.4308
Pancreas	0.0099	0.0055	1.7949	0.5571
Prostate	0.0066	0.0065	1.0129	0.9872
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0034	0.0000	undef	0.0000
Hematopoietic	0.0053			
Penis	0.0080			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0243
White blood cells	0.0000

Electronic Northern for Seq. ID: 225

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0136	0.5519 1.8120
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0053	0.0056	0.9393 1.0646
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0072	0.8296 1.2055
Endocrine tissue	0.0177	0.0018	9.9589 0.1004
Brain	0.0075	0.0050	1.5087 0.6628
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0088	0.0111	0.7893 1.2669
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0074	0.4639 2.1557
Kidney	0.0090	0.0048	1.8570 0.5385
Pancreas	0.0099	0.0055	1.7949 0.5571
Prostate	0.0113	0.0013	8.6822 0.1152
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0059	0.0046	1.2851 0.7781
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0127
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 226

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0023	0.0000	undef
Breast	0.0053	0.0056	0.9393	1.0646
Large intestine	0.0057	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0016	0.0053	0.3018	3.3136
Brain	0.0035	0.0020	1.7408	0.5745
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0059	0.0000	undef
Lung	0.0019	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0045	0.0048	0.9285	1.0770
Pancreas	0.0033	0.0000	undef	0.0000
Prostate	0.0038	0.0000	undef	0.0000
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0059	0.0046	1.2851	0.7791
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0000			
Seminal vesicle	0.0080			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0182
Sensory organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 227

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0038	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0025	0.0089	0.2799 3.5727
Large intestine	0.0057	0.0228	0.2523 3.9638
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0059	0.0095	0.6222 1.6073
Endocrine tissue	0.0096	0.0033	2.9275 0.3416
Brain	0.0134	0.0050	2.6904 0.3717
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0093	0.0063	1.4649 0.6826
Heart	0.0081	0.0137	0.5907 1.6928
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0049	0.0037	1.3158 0.7600
Stomach-esophagus	0.0000	0.0165	0.0000 undef
Muscle-skeleton	0.0000	0.0074	0.0000 undef
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0033	0.0092	0.3604 2.7748
Prostate	0.0113	0.0078	1.4470 0.6911
T lymphoma	0.0033	0.0173	0.1901 5.2613
Uterus	0.0118	0.0046	2.5702 0.3891
White blood cells	0.0023	0.0000	undef 0.0000
Hematopoietic	0.0047		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0279
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0108
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0125
Ovary t	0.0379
Endocrine tissue	0.0000
Fetal	0.0066
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0090
Testicles_n	0.0169
Testicles_t	0.0228
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0191
Kidney t	0.0495
Ovary uterus	0.0325
Prostate n	0.0182
Sensory organs	0.0077

Electronic Northern for Seq. ID: 228

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0094	0.0000	undef
Breast	0.0070	0.0056	1.2524	0.7985
Large intestine	0.0057	0.0000	undef	0.0000
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0148	0.0048	3.1108	0.3215
Endocrine tissue	0.0016	0.0018	0.9054	1.1045
Brain	0.0064	0.0060	1.0638	0.9400
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0127	0.0000	undef
Heart	0.0030	0.0000	undef	0.0000
Testicles	0.0080	0.0118	0.6786	1.4737
Lung	0.0019	0.0074	0.2631	3.8007
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0057	0.0026	2.1706	0.4607
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0015	0.0046	0.3213	3.1125
White blood cells	0.0048	0.0000	undef	0.0000
Hematopoietic	0.0067			
Penis	0.0027			
Seminal vesicle	0.0070			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary uterus	0.0023
Prostate_n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 229

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0039	0.0023	1.6595	0.6026
Breast	0.0018	0.0000	undef	0.0000
Large intestine	0.0019	0.0028	0.6728	1.4864
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0016	0.0000	undef	0.0000
Brain	0.0000	0.0020	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0059	0.0000	undef
Stomach-esophagus	0.0010	0.0018	0.5262	1.9004
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0037	0.4639	2.1557
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0017	0.0000	undef	0.0000
T lymphoma	0.0038	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0027			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0121
White blood cells	0.0000

Electronic Northern for Seq. ID: 230

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0136	0.3679 2.7181
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0053	0.0042	1.2524 0.7985
Large intestine	0.0038	0.0057	0.6728 1.4864
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0148	0.0072	2.0739 0.4822
Endocrine tissue	0.0080	0.0106	0.7545 1.3254
Brain	0.0046	0.0060	0.7737 1.2925
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0041	0.0000	undef 0.0000
Testicles	0.0120	0.0000	undef 0.0000
Lung	0.0010	0.0018	0.5262 1.9004
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0185	0.4639 2.1557
Kidney	0.0022	0.0048	0.4642 2.1540
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0019	0.0013	1.4470 0.6911
T lymphoma	0.0000	0.0075	0.0000 undef
Uterus	0.0015	0.0230	0.0643 15.5627
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0100
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0182
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 231

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0117	0.0047	2.4892 0.4017
Breast	0.0053	0.0028	1.8786 0.5323
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0110	0.0213	0.5153 1.9406
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0064	0.0053	1.2071 0.8284
Brain	0.0064	0.0140	0.4559 2.1934
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0254	0.0000 undef
Heart	0.0000	0.0137	0.0000 undef
Testicles	0.0000	0.0059	0.0000 undef
Lung	0.0068	0.0055	1.2278 0.8144
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0067	0.0096	0.6964 1.4360
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0104	0.0039	2.6529 0.3769
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0080		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0418
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 232

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0136	0.7358	1.3590
Bladder	0.0117	0.0094	1.2446	0.8035
Breast	0.0150	0.0056	2.6614	0.3757
Large intestine	0.0038	0.0199	0.1922	5.2023
Small intestine	0.0110	0.0000	undef	0.0000
Ovary	0.0119	0.0215	0.5530	1.8082
Endocrine tissue	0.0048	0.0053	0.9054	1.1045
Brain	0.0046	0.0040	1.1605	0.8617
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0046	0.0190	0.2441	4.0959
Heart	0.0142	0.0137	1.0337	0.9674
Testicles	0.0080	0.0118	0.6786	1.4737
Lung	0.0078	0.0092	0.8419	1.1877
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0034	0.0074	0.4639	2.1557
Kidney	0.0067	0.0096	0.6964	1.4360
Pancreas	0.0066	0.0000	undef	0.0000
Prostate	0.0123	0.0039	3.1353	0.3190
T lymphoma	0.0101	0.0224	0.4508	2.2182
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0062	0.0000	undef	0.0000
Hematopoietic	0.0134			
Penis	0.0134			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0245
Fetal	0.0087
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0100
Kidney t	0.0000
Ovary uterus	0.0338
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 233

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0117	0.6638 1.5065
Breast	0.0088	0.0155	0.5693 1.7566
Large intestine	0.0211	0.0028	7.4006 0.1351
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0119	0.0024	4.9773 0.2009
Endocrine tissue	0.0032	0.0142	0.2263 4.4181
Brain	0.0035	0.0000	undef 0.0000
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0279	0.0000	undef 0.0000
Heart	0.0071	0.0137	0.5169 1.9347
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0292	0.0148	1.9733 0.5068
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0269	0.0000	undef 0.0000
Pancreas	0.0165	0.0000	undef 0.0000
Prostate	0.0141	0.0052	2.7132 0.3686
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0040		
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0145
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0068
Prostate_n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 234

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0035	0.0056	0.6262 1.5969
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0000	undef 0.0000
Endocrine tissue	0.0048	0.0018	2.7161 0.3682
Brain	0.0035	0.0010	3.4816 0.2872
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0020	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0049	0.0000	undef 0.0000
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0037	0.4639 2.1557
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0038	0.0000	undef 0.0000
T lymphoma	0.0126	0.0000	undef 0.0000
Uterus	0.0074	0.0046	1.6064 0.6225
White blood cells	0.0059	0.0304	0.1803 5.5448
Hematopoietic	0.0013		
Penis	0.0000		
Seminal vesicle	0.0141		
Sensory organs	0.0000		

	FETUS % freq.
Development	0.0139
Gastrointestinal	0.0139
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0113
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 235

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0136	0.0000	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0014	0.0000	undef
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0107	0.0000	undef
Ovary	0.0059	0.0048	1.2443	0.8036
Endocrine tissue	0.0016	0.0053	0.3018	3.3136
Brain	0.0006	0.0030	0.1934	5.1701
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0019	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0038	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0046	0.0000	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0027			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 236

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0194	0.0084	2.2961	0.4355
Large intestine	0.0096	0.0000	undef	0.0000
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0059	0.0024	2.4887	0.4018
Endocrine tissue	0.0128	0.0053	2.4143	0.4142
Brain	0.0041	0.0070	0.5803	1.7234
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0058	0.0092	0.6315	1.5836
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0090	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Prostate	0.0104	0.0039	2.6529	0.3769
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0118	0.0000	undef	0.0000
White blood cells	0.0089	0.0000	undef	0.0000
Hematopoietic	0.0134			
Penis	0.0080			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0176	0.0070	2.5048 0.3992
Large intestine	0.0077	0.0057	1.3456 0.7432
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0032	0.0035	0.9054 1.1045
Brain	0.0069	0.0010	6.9631 0.1436
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0061	0.0137	0.4430 2.2572
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0029	0.0037	0.7893 1.2669
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0037	0.0000 undef
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0085	0.0026	3.2558 0.3071
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0074	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
	0.0118		
FETUS			
	% freq.		
Development	0.0000		
Gastrointestinal	0.0056		
Brain	0.0000		
Hematopoietic	0.0079		
Skin	0.0000		
Hepatic	0.0520		
Heart-blood vessels	0.0036		
Lung	0.0072		
Adrenal gland	0.0000		
Kidney	0.0062		
Placenta	0.0000		
Prostate	0.0000		
Sensory organs	0.0000		

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles n	0.0084
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary uterus	0.0203
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 238

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0075	0.0000	undef	0.0000
Bladder	0.0000	0.0047	0.0000	undef
Breast	0.0009	0.0014	0.6262	1.5969
Large intestine	0.0019	0.0028	0.6728	1.4864
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0148	0.0024	6.2217	0.1607
Endocrine tissue	0.0016	0.0018	0.9054	1.1045
Brain	0.0017	0.0060	0.2901	3.4467
Skin	0.0037	0.0789	0.0466	21.4787
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0120	0.0118	1.0178	0.9825
Lung	0.0029	0.0018	1.5786	0.6335
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0113	0.0026	4.3411	0.2304
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0030	0.0092	0.3213	3.1125
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0040			
Penis	0.0027			
Seminal vesicle	0.0070			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 239

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0000	undef 0.0000
Bladder	0.0156	0.0094	1.6595 0.6026
Breast	0.0141	0.0225	0.6262 1.5969
Large intestine	0.0172	0.0085	2.0184 0.4955
Small intestine	0.0192	0.0213	0.9018 1.1089
Ovary	0.0237	0.0262	0.9050 1.1050
Endocrine tissue	0.0144	0.0160	0.9054 1.1045
Brain	0.0197	0.0269	0.7307 1.3686
Skin	0.0184	0.0000	undef 0.0000
Hepatic	0.0279	0.0190	1.4649 0.6826
Heart	0.0203	0.0275	0.7384 1.3543
Testicles	0.0040	0.0059	0.6786 1.4737
Lung	0.0175	0.0166	1.0524 0.9502
Stomach-esophagus	0.0217	0.0000	undef 0.0000
Muscle-skeleton	0.0103	0.0037	2.7833 0.3593
Kidney	0.0112	0.0289	0.3869 2.5849
Pancreas	0.0116	0.0055	2.0941 0.4775
Prostate	0.0141	0.0039	3.6176 0.2764
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0148	0.0184	0.8032 1.2450
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0125
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0213
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0168
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0261
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 240

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0023	0.0000	undef
Breast	0.0035	0.0014	2.5048	0.3992
Large intestine	0.0019	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0041	0.0020	2.0309	0.4924
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0137	0.0738	13.5431
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0034	0.0037	0.9276	1.0778
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0057	0.0039	1.4470	0.6911
Uterus	0.0126	0.0000	undef	0.0000
White blood cells	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0062	0.0000	undef	0.0000
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0485
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 241

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0070	0.0098	0.7157	1.3973
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0320	0.0000	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0032	0.0000	undef	0.0000
Brain	0.0012	0.0199	0.0580	17.2337
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0061	0.0000	undef	0.0000
Lung	0.0080	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0064	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0045	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0085	0.0052	1.6279	0.6143
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0103	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000			
Sensory organs	0.0107			
	0.0000			
	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary uterus	0.0180
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 242

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0047	0.0000	undef
Breast	0.0018	0.0028	0.6262	1.5969
Large intestine	0.0057	0.0028	2.0184	0.4955
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0048	0.0035	1.3580	0.7364
Brain	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	0.0000
Testicles	0.0030	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0128	0.0000	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0057	0.0026	2.1706	0.4607
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0030	0.0046	0.6426	1.5563
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 243

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0014	1.8786	0.5323
Large intestine	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0059	0.0000	undef	0.0000
Endocrine tissue	0.0032	0.0071	0.4527	2.2091
Brain	0.0012	0.0090	0.1289	7.7552
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0029	0.0018	1.5786	0.6335
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0047	0.0013	3.6176	0.2764
Uterus	0.0025	0.0000	undef	0.0000
White blood cells	0.0030	0.0092	0.3213	3.1125
Hematopoietic	0.0021	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary Uterus	0.0180
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 244

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0117	0.0117	0.9957	1.0043
Breast	0.0097	0.0070	1.3777	0.7259
Large intestine	0.0077	0.0000	undef	0.0000
Small intestine	0.0165	0.0000	undef	0.0000
Ovary	0.0000	0.0048	0.0000	undef
Endocrine tissue	0.0080	0.0071	1.1317	0.8836
Brain	0.0075	0.0080	0.9429	1.0605
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0063	0.7324	1.3653
Heart	0.0071	0.0000	undef	0.0000
Testicles	0.0120	0.0059	2.0357	0.4912
Lung	0.0049	0.0000	undef	0.0000
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0171	0.0111	1.5463	0.6467
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0050	0.0166	0.2992	3.3427
Prostate	0.0198	0.0078	2.5323	0.3949
T lymphoma	0.0051	0.0149	0.3381	2.9576
Uterus	0.0163	0.0046	3.5341	0.2830
White blood cells	0.0123	0.0000	undef	0.0000
Hematopoietic	0.0053			
Penis	0.0054			
Seminal vesicle	0.0141			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0081
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 245

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0117	0.0117	0.9957	1.0043
Breast	0.0132	0.0084	1.5655	0.6388
Large intestine	0.0134	0.0028	4.7095	0.2123
Small intestine	0.0027	0.0107	0.2577	3.8812
Ovary	0.0030	0.0072	0.4148	2.4109
Endocrine tissue	0.0032	0.0106	0.3018	3.3136
Brain	0.0156	0.0070	2.2381	0.4468
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0093	0.0000	undef	0.0000
Heart	0.0122	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0117	0.0037	3.1573	0.3167
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0045	0.0048	0.9285	1.0770
Pancreas	0.0033	0.0110	0.2992	3.3427
Prostate	0.0207	0.0000	undef	0.0000
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0089	0.0138	0.6426	1.5563
White blood cells	0.0055	0.0607	0.0902	11.0896
Hematopoietic	0.0000			
Penis	0.0134			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0080
Kidney_t	0.0000
Ovary uterus	0.0135
Prostate_n	0.0061
Sensory organs	0.0387
White blood cells	0.0000

Electronic Northern for Seq. ID: 246

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0141	0.0000	undef
Breast	0.0000	0.0042	0.0000	undef
Large intestine	0.0115	0.0028	4.0367	0.2477
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0048	0.0053	0.9054	1.1045
Brain	0.0064	0.0030	2.1276	0.4700
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0161	0.0059	2.7142	0.3684
Lung	0.0058	0.0074	0.7893	1.2669
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0055	0.2992	3.3427
Prostate	0.0057	0.0026	2.1706	0.4607
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0044	0.0000	undef	0.0000
White blood cells	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0107			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0195
Nerves	0.0000
Kidney t	0.0050
Ovary uterus	0.0000
Prostate_n	0.0068
Sensory organs	0.0182
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 247

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0136	0.1840 5.4361
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0106	0.0056	1.8786 0.5323
Large intestine	0.0096	0.0142	0.6728 1.4864
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0048	0.6222 1.6073
Endocrine tissue	0.0016	0.0231	0.0696 14.3590
Brain	0.0139	0.0040	3.4816 0.2872
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0127	0.7324 1.3653
Heart	0.0081	0.0275	0.2954 3.3858
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0078	0.0092	0.8419 1.1877
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0112	0.0145	0.7737 1.2924
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0113	0.0065	1.7364 0.5759
T lymphoma	0.0152	0.0224	0.6762 1.4788
Uterus	0.0059	0.0000	undef 0.0000
White blood cells	0.0096	0.0607	0.1578 6.3369
Hematopoietic	0.0094		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0371
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0156
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0181
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0121
Sensory organs	0.0232
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S . If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST.
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K.F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S . Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i: iteration index) obtained each time until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above described examples, it was possible to find the nucleic acid sequences described in Table I from prostate tumor tissue.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4

Mapping of nucleic acid sequences on the human genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker which is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7; 541-550). The database used here no longer corresponds to the one cited in the literature, but is a development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/index.html>). Analogously to the mapping by the hybrid panels, the results were

evaluated with the aforementioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq.ID No.	Identified BACs		
3	320-L-23		
4	461-O-11		
8	283-P-15	322-B-7	317-H-19
24	272-N-9	340-L-19	554-D-3
31	293-K-21	337-I-17	363-J-15
46	410-A-9		
47	268-B-2	532-B-10	

Table 1

Col. 1 - Seq ID
 Col. 2 - Expression
 Col. 3 - Function
 Col. 4 - Modules
 Col. 5 - Cytogenetic localization
 Col. 6 - Nearest marker
 Col. 7 - Length of initial EST in bases
 Col. 8 - Length of claimed sequence in bases
 Col. 9 - Seq ID of initial sequence

Tabelle 1

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
2	im normalen Prostatagewebe erhöht	ZYXIN 2	LIM	7q33-7q35	D7S661	202	1437	
3	in gesundem Prostata- und Brustgewebe erhöht	Unbekannt		17p13.3	D17S2199-D17S1548	207	707	
4	im normalen Prostatagewebe erhöht	PCCMT		1p36.31	D1S2145-D1S2132	215	1265	
6	im normalen Prostatagewebe erhöht	Unbekannt	UBIQUITIN_CONJUGAT_2	1q21.2	D1S3384-D1S305	225	1330	
7	im normalen Prostatagewebe erhöht	Unbekannt		11q11-q13.1	D11S4205-D11S4535	231	762	
8	im normalen Prostatagewebe erhöht	Humanes Homolog des TEGT-Proteins aus der Ratte		10q23.1	D10S551-D10S532	246	1228	
9	im normalen Blasen- und Prostatagewebe erhöht	SRP20	rrm	6p21.2	NIB1566-WI-4186	243	914	
10	4x stärker als im normalen Prostatagewebe	Muf1		1p33-p32.3	D1S1558-D1S232	315	1126	
12	im normalen Prostatagewebe erhöht	Unbekannt		7p21.3-7p14.1	D7S2363	219	538	
13	im normalen Prostatagewebe erhöht	Unbekannt		22q12.1 - 22q13.1	D22S1144	210	321	
14	ausschließlich in der normalen Prostata	E4BP4	B_ZIP	9q22.1-q22.2	D9S787	217	847	
16	stärker im normalen Brust- und Prostatagewebe als im entsprechenden Tumor	HUMANer PHOSPHOLEMMAN PRECURSOR		19q13.1		210	573	
17	verstärkt in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Mögliches Humans Homolog zu S1R		12q13.13 - 12q14.1	D12S1700-D12S1601	244	486	

Table 1

Seq ID	Expression	Function
2	elevated in normal prostate tissue	ZYXIN 2
3	elevated in healthy prostate and breast tissue	Unknown
4	elevated in normal prostate tissue	PCCMT
6	elevated in normal prostate tissue	Unknown
7	elevated in normal prostate tissue	Unknown
8	elevated in normal prostate tissue	Human homolog of TEGT protein from rats
9	elevated in normal bladder and prostate tissue	SRP20
10	4x more heavily than in normal prostate tissue	Muf1
12	elevated in normal prostate tissue	Unknown
13	elevated in normal prostate tissue	Unknown
14	solely in normal prostate	E4BP4
16	more heavily in normal breast and prostate tissue than in the corresponding tumor	HUMAN PHOSPHOLEMMAN PRECURSOR
17	intensified in normal prostate, compared to corresponding tumor tissue	Possible human homolog to S1R

UBIQUITIN_CONJUGAT_2 = UBIQUITIN_CONJUGATE_2

Seq ID	Expression	Function
18	about 6x more heavily in normal prostate compared to corresponding tumor tissue	Unknown
19	about 2x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
21	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 7x more often in breast and lung tumors than in corresponding normal tissue	Homolog to JANUS-A from <i>Drosophila melanogaster</i>
23	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
24	5x more heavily in normal prostate tissue than in corresponding tumor tissue, strongly expressed in skin tumors	E1F-6

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
18	ca. 6x stärker in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Unbekannt		10q23.32 - 10q24.31	D10S551-D10S532	215	662	
19	ca. 2x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		2q35	D2S433-D2S295	225	750	
21	ca. 3x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe, ca. 7x häufiger in Brust- und Lungentumoren als in entsprechenden Normalgeweben	Homolog zu JANUS-A aus <i>Drosophila melanogaster</i>		9q34.13	D9S158-D9S2053	229	1001	
23	stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		1p36.13-p32.3	SGC32968	184	580	
24	5x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe, stark exprimiert in Hauttumoren	E1F-6		20q11.1-q11.22		237	740	

Seq ID	Expression	Function
26	more heavily in normal prostate tissue than in corresponding tumor tissue	Homolog to HUMAN SORCIN
27	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
28	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
29	more heavily in normal prostate tissue than in corresponding tumor tissue	IL-6SAG
30	about 4x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
31	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
32	more heavily in normal prostate tissue than in corresponding tumor tissue, elevated 10x in muscle and skeletal tumors	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
26	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Homolog zu HUMANem SORCIN		1p36 11-p34 3	D1S233-D1S2548	219	975	
27	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		9p21 1-9q12	SHGC-7278-SHGC-33912	259	854	
28	ca. 3x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		11q12 1-11q13 5	SHGC-15247-NIB715	288	802	
29	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	IL-6SAG		20p11 23-p11 21	D20S807-SHGC-11944	224	807	
30	ca. 4x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		Xp11 23-p11 21	WI-5587-WI-5717	276	777	
31	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt				238	501	
32	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe, 10x erhöht in Muskel- und Skelettumoren	Unbekannt		3p21 1 - 3p22 2	WI-9590-WI-3521	284	1104	

Seq. ID	Expression	Function
33	elevated in normal prostate tissue	Human homolog of WW-domain binding protein 1 from mice
35	elevated in normal prostate tissue and in gastrointestinal tumors	Unknown
36	elevated in normal prostate tissue	Id1
37	elevated in normal prostate tissue	Unknown
39	elevated in prostate tumors	C1 inhibitor
41	more heavily in normal prostate tissue than in corresponding tumor tissue	Acyl-protein thioesterase
42	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
43	about 6x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
33	in normalem Prostatagewebe erhöht	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085	208	810	
35	in normalem Prostatagewebe und in gastrointestinalen Tumoren erhöht	Unbekannt		3p23-p21.1	SHGC-32684-D3S4150	223	826	
36	in normalem Prostatagewebe erhöht	Id1	HLH	20p11.22 - 20q11.21	WI-1163	254	578	
37	in normalem Prostatagewebe erhöht	Unbekannt		8p12	SHGC-5722-SHGC-5765	293	799	
39	in Prostata Tumoren erhöht	C1 inhibitor	serpin	11p13-11q13.1	SHGC-30227-D11S1983	262	1743	
41	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Acyl-protein thioesterase		6p21.31-q21.2	D6S1868-D6S1867	267	1183	
42	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		16q12.1-22.1	SHGC-6119-SHGC-15371	270	768	
43	ca. 6x stärker in normalem Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		17q11.2-q21.31	SHGC-30259-SHGC-13493	279	1029	

Seq. ID	Expression	Function
44	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 8x more often in a brain tumor than in comparable normal tissue	Unknown
46	elevated in normal prostate tissue	Unknown
47	elevated in normal prostatic, hepatic and ovarian tissue	Unknown
51	elevated in normal prostate tissue and hematopoietic tumors	Unknown
52	elevated in normal prostate tissue and in brain tumors	SPARC
53	elevated in normal prostate tissue	Unknown
54	elevated in normal prostate tissue and in skeletal tumors	Unknown
55	elevated in normal prostate tissue and hepatic tumors	B4-2

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
44	ca. 3x starker in normalem Prostata-gewebe als im entsprechenden Tumorgewebe, ca. 8x häufiger im Gehirntumor als im vergleichbaren Normalgewebe	Unbekannt		16q23 1-q24 2	SHGC-32665-SHGC-11833	237	736	
46	in normalem Prostata-gewebe erhöht	Unbekannt		19p13 3	IB1264-WI-6480	259	1159	
47	in normalem prostatäischem, hepatischen und ovarial Gewebe erhöht	Unbekannt		6q13-q21		159	690	
51	in normalem Prostata-gewebe und in haematopoetischen Tumoren erhöht	Unbekannt		1p36 11	D1S3131-D1S2674	250	1186	
52	in normalem Prostata-gewebe und in Gehirntumoren erhöht	SPARC	kazal	5q21 1-q33.2	WI-7565-WI-6351	261	1029	
53	in normalem Prostata-gewebe erhöht	Unbekannt		15q23-24.1	D15S1241-D15S197	261	985	
54	in normalem Prostata-gewebe und in Skelettumoren erhöht	Unbekannt		4p14	D4S405-SHGC-9448	246	622	
55	in normalem Prostata-gewebe und hepatischen Tumoren erhöht	B4-2		6q16.2	D6S1644-D6S2057	239	1129	

Seq. ID	Expression	Function
58	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
59	about 5x more heavily in normal prostate tissue than in corresponding tumor tissue	Methyl-CpG binding protein MBD2
60	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
61	elevated in normal prostate tissue and in endocrine tumors	Unknown
62	elevated in normal prostate and breast tissue	Unknown
63	elevated in normal prostate, bladder and breast tumors	Unknown
64	expressed 1.8088x in benign prostate tissue	Homolog to RanBP7
217	expressed 2.894x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nachster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
58	ca. 3x stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		1q12	SHGC-32015-D1S442	160	877	
59	ca. 5x stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Methyl-CpG bindendes Protein MBD2		18q21 32-18q21 32		288	1329	
60	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		11q21-11q23 2		310	697	
61	in normalem Prostatagewebe und in endokrinen Tumoren erhöht	Unbekannt		17p11 2	AFMA126YD5	378	1389	
62	in normalem Prostata- und Brustgewebe erhöht	Unbekannt		4q21 21 - 4q21.23	WI-7565-WI-9200	260	535	
63	in normalem Prostata-, Blasen- und Brusttumoren erhöht	Unbekannt		16p12 3 - 16p13 11	AFMB354YF9	216	1098	
64	1.8088 x im gutartigen Prostatagewebe exprimiert	Homolog zu RanBP7		11p15 3-p15.5	D11S909-D11S4149	302	1860	
217	2.894 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt	UBIQUITIN_CON JUGAT	1q21.2	D1S3384-D1S305		1880	6

Seq ID	Expression	Function
218	expressed 2.1705x in benign prostate tissue compared to the prostate tumor	Unknown
219	expressed 2.7494x in benign prostate tissue compared to the prostate tumor	Human homolog of TEGT from rats
220	expressed 2.46x in benign prostate tissue compared to the prostate tumor	TXBP151
221	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Possible human homolog to S1R
222	expressed 2.8941x in benign prostate tissue compared to the prostate tumor	Unknown
223	expressed 0.8348x in benign prostate tissue compared to the prostate tumor	Homolog to HYA22
224	expressed 1.0129x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nachster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
218	2.1705 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		11q11-q13 1	D11S4205-D11S4535		1024	7
219	2.7494 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Humanes Homolog des TEGT aus der Ratte		10q23 1	D10S551-D10S532		2383	8
220	2.46 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	TXBP151	COILS	7p21 3-7p14 1	D7S2363		3210	12
221	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Mögliches Humans Homolog zu S1R		12q13 13 - 12q14 1	D12S1700-D12S1601		1030	17
222	2.8941 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		10q23 32 - 10q24 31	D10S551-D10S532		1216	18
223	0.8348 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Homolog zu HYA22		2q35	D2S433-D2S295		2369	19
224	1.0129 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1p36 13-p32 3	SGC32968		849	23

Seq. ID	Expression	Function
225	expressed 8.6822x in benign prostate tissue compared to the prostate tumor	Homolog to HUMAN SORCIN
226	No similar sequence was found in the prostate tumor	Unknown
227	expressed 2.4117x in benign prostate tissue compared to the prostate tumor	IL-6SAG
228	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
229	No similar sequence was found in the prostate tumor	Unknown
230	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown
231	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Human homolog of WW-domain binding protein 1 from mice
232	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	Homolog to OLIGOSACCHARYL TRANSFERASE STT3 subunit from <i>C. elegans</i>

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
225	8.6822 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Homolog zu HUMANem SORCIN	EF_HAND_2	1p36.11-p34.3	D1S233-D1S2548		1502	26
226	Es wurde keine ähnliche Sequenz im Prostata-tumor gefunden	Unbekannt		9p21.1-9q12	SHGC-7278-SHGC-33912		1892	27
227	2.4117 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	IL-6SAG		20p11.23-p11.21	D20S807-SHGC-11944		1522	29
228	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		Xp11.23-p11.21	WI-5587-WI-5717		2016	30
229	Es wurde keine ähnliche Sequenz im Prostata-tumor gefunden	Unbekannt					765	31
230	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Unbekannt		3p21.1 - 3p22.2	WI-9590-WI-3521		1611	32
231	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085		1473	33
232	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostata-tumor exprimiert	Homolog zu der OLIGOSACCHARYL TRANSFERASE STT3 Untereinheit aus <i>C. elegans</i>		3p23-p21.1	SHGC-32684-D3S4150		2503	35

Seq. ID	Expression	Function
233	expressed 2.7132x in benign prostate tissue compared to the prostate tumor	Unknown
234	No similar sequence was found in the prostate tumor	Acyl-protein thioesterase
235	No similar sequence was found in the prostate tumor	Unknown
236	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Stat5b
237	expressed 3.2558x in benign prostate tissue compared to the prostate tumor	Unknown
238	expressed 4.3411x in benign prostate tissue compared to the prostate tumor	Unknown
239	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	SDP3
240	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
233	2.7132 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		8p12	SHGC-5722-SHGC-5765		1756	37
234	Es wurde kein ähnliche Sequenz im Prostata tumor gefunden	Acyl-protein thioesterase		6p21 31-q21 2	D6S1868-D6S1867		1286	41
235	Es wurde kein ähnliche Sequenz im Prostata tumor gefunden	Unbekannt		16q12 1-22 1	SHGC-6119-SHGC-15371		1230	42
236	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Stat5b		17q11 2-q21 31	SHGC-30259-SHGC-13493		2328	43
237	3.2558 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		16q23 1-q24 2	SHGC-32665-SHGC-11833		1767	44
238	4.3411 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		19p13 3	IB1264-WI-6480		2311	46
239	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	SDP3	PX	6q13-q21			1772	47
240	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1p36 11	D1S3131-D1S2674		2409	51

Seq ID	Expression	Function
241	expressed 1.6279x in benign prostate tissue compared to the prostate tumor	Unknown
242	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
243	expressed 3.6176x in benign prostate tissue compared to the prostate tumor	Unknown
244	expressed 2.5323x in benign prostate tissue compared to the prostate tumor	Unknown
245	No similar sequence was found in the prostate tumor	LIMP II
246	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
247	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Homolog to RanBP7

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nachster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
241	1.6279 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		15q23-24 1	D15S1241-D15S197		2594	53
242	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		4p14	D4S405-SHGC-9448		1012	54
243	3.6176 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1q12	SHGC-32015-D1S442		1206	58
244	2.5323 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		17p11 2	AFMA126YD5		2514	61
245	Es wurde kein ähnliche Sequenz im Prostata tumor gefunden	LIMP II	CD36	4q21.21 - 4q21 23	WI-7565-WI-9200		3903	62
246	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		16p12 3 - 16p13 11	AFMB354YF9		1730	63
247	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Homolog zu RanBP7		11p15 3-p15 5	D11S909-D11S4149		3439	64

Table 2

<u>DNA Sequence</u> <u>ID No.</u>	<u>ORF Sequence ID No.</u>						
2	66						
3	67	68	69	70			
4	71						
6	73						
7	74						
8	75						
9	82						
10	83						
12	90						
14	91						
16	92						
17	93						
18	97	98	99	100	101		
19	102	103	104	105			
21	109						
23	111	112	113				
24	114						
26	116						
27	117	118	119				
28	120	121	122	123	124		
29	128						
30	129	130	131				
31	132						
32	133						
33	134	135	136	137			
35	139	140	141	142	143	144	145
36	147	148	149				146
39	152						
41	154	155	156	157			
42	158	159	160	161			
43	162	163	164				
44	165						
46	168	169	170	171	172		
47	173						
51	183	184	185	186	187		
52	188	189	190	191	192	193	
54	194						
55	195						
58	201						
59	202	203	204	205	206		
60	207	208	209				
61	210						
62	214	215	216				
217	248						
218	249	250					
219	251						
220	252						
221	253						

<u>DNA Sequence</u>	<u>ORF Sequence</u>
<u>ID No.</u>	<u>ID No.</u>

222	254 255
223	256
224	257
225	258
226	259 260
227	261 262
228	263
229	264 265
230	266
231	267 268
232	269
233	270 271
234	272 273
235	274 275
236	276
237	277 278
238	280 281
239	282
240	283 284
241	285 286
242	287 288
243	289 290
244	291 292
245	293
246	294
247	295

The inventive nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 are described in the following sequence protocol.

Sequence protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft fuer Genomforschung mbH
- (B) STREET: Ihnestrassse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP) D-14195
- (G) TELEPHONE: (030)-8413 1672
- (H) FAX: (030)-8413 1671

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Prostate Tissue

(iii) Number of sequences: 216

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0 version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 2:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1437 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

CTCCTTGGAA GTCCCCTTCC AGCTCCCAGC CTCTGCCCCA GGTTCGGGCT CCGGCTCAGA 60
GCCAGACACA GTTCCATGTT CAGCCCCAGC CCCAGCCCCA GCCTCAGGTC CAACTCCATG 120
TCCAGTCCCA GACCCAGCCT GTGTCTTTGG CTAACACCCA GCCCCGAGGG CCCCAGCCT 180
CATCTCCGGC TCCAGCCCCCT AAGTTTTTCTC CAGTGACTCC TAAGTTTACT CCTGTGGCTT 240
CCAAGTTCAG TCCTGGAGCC CCAGGTGGAT CTGGGTCACA ACCAAATCAA AAATTGGGGC 300
ACCCCGAAGC TCTTTCTGCT GGCACAGGCT CCCCTCAACC TCCCAGCTTC ACCTATGCCC 360
AGCAGAGGGA GAAGCCCCGA GTGCAGGAGA AGCAGCACCC CGTGCCCCCA CCGGCTCAGA 420
ACCAAAACCA GGTGCGCTCC CCTGGGGGCC CAGGGCCCCT GACTCTGAAG GAGGTGGAGG 480
AGCTGGAGCA GCTGACCCAG CAGCTAATGC AGGACATGGA GCATCCTCAG AGGCAGAATG 540
TGGCTGTCAA CGAACTCTGC GGCCGATGCC ATCAACCCCT GGCCCGGGCG CAGCAGCCGT 600
CCGCGCTCTA GGGCAGCTGT TCCACATCGC CTGCTTCACC TGCCACCAGT GTGCGCAGAG 660
CTCCAGGGCC AGCAGTTCTA TCTCTGGAG GGGGCGCCGT ACTGCGAGGG CTGTTACACT 720
GACACCCTGG AGAAGTGTAT TGC GGGG GAGCCCATCA CTGACCGCAT GCTGAGGGCC 780
ACGGGCAAGG CCTATCACCC GACTGCTTC ACCTGTGTGG TCTGCGCCCG CCCCCTGGAG 840
GGCACCTCCT TCATCGTGGA CCAGGCCAAC CGGCCCACT GTGTCCCCGA CTACCACAAG 900
CAGTACGCCC CGAGGTGCTC CGTCTGCTCT GAGCCCATCA TGCCTGAGCC TGGCCGAGAT 960
GAGACTGTGC GAGTGGTCTC CCTGGACAAG AACTTCCACA TGAAGTGTTA CAAGTGTGAG 1020
GACTGCGGGA AGCCCCTGTC GATTGAGGCA GATGACAATG GCTGCTTCCC CCTGGACGGT 1080
CACGTGCTCT GTCGGAAGTG CCACACTGCT AGAGCCCA GA CCTGAGTGAG GACAGGCCCT 1140
CTTCAGACCG CAGTCCATGC CCCATTGTGG ACCACCCACA CTGAGACCAC CTGCCCCCAC 1200
CTCAGTTATT GTTTTGATGT CTAGCCCCTC CCATTTCCTA CCCCTCCCTA GCATCCCAGG 1260
TGCCCTGACC CAGGACCCAA CATGGTCTAG GGATGCAGGA TCCCCGCCCT GGGGTCTGGT 1320
CCTCGCCCAT CCTGCAGGGA TTGCCACCG TCTTCCAGAC ACCCCACCTG AGGGGGGCAC 1380
AAGGTTTAGT GCTGCTGCTT TCACTGCTGC ACCCGCGCCC TCGGCCGGCC CCCCAG 1437

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 707 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCCCCG	GCCTTAAAGC	GTCCATTTCC	CAGCGGCCCT	CCGCTGCGAG	ACCGCAGCCC	60
TTCTCTGGAG	TCTCAGAGCC	GCAAGACACC	ACGACTCCCA	GAGGACCTTG	CGTCGGGCAA	120
GAAAGACTAC	ACCTTCCAGA	GGCCTCTGCG	GCGCCGCGAC	AGGAAGCGGC	GGGCGAGCCG	180
AGTGTCTTGG	CGCGTGGATC	CGAGCGACCA	TGGTGGCCCC	GGTGTGGTCG	CTGATGAGGT	240
TCCTCATCAA	GGGAAGTGTG	GCTGGGGGCG	CCGTCTACCT	GGTGTACGAC	CAGGAGCTGC	300
TGGGGCCCAG	CGACAAGAGC	CAGGCAGCCC	TACAGAAGGC	TGGGGAGGTG	GTCCCCCCCC	360
CCATGTACCA	GTTCAGCCAG	TACGTGTGTC	AGCAGACAGG	CCTGCAGATA	CCCCAGCTCC	420
CAGCCCCTCC	AAAGATTTAC	TTTCCCATCC	GTGACTCCTG	GAATGCAGGC	ATCATGACGG	480
TGATGTCAGC	TCTGTCGGTG	GCCCCCTCCA	AGGCCCGCGA	GTACTCCAAG	GAGGGCTGGG	540
AGTATGTGAA	GGCGCGCACC	AAGTAGCGAG	TCAGCAGGGC	CGCCTGCCCC	GGCCAGAACG	600
GGCAGGGCTG	CCACTGACCT	GAAGACTCCG	GACTGGGACC	CCACTCCGAG	GGCAGGCCTC	660
CCGATTGCCG	GCCCAATAAA	GGACTTCAGA	AGTGAAAAAA	AAAAAAA		707

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

CACTGGGATG GGCATACACT ACTCACAGGG TGTGTGAGAT GAGAAGAACA CGTCAANGTT 60
TTTATACTCA GATGTGGGAG CGACATCAAT GAAATCTGTA CTGTATGAAA GCTACACAAA 120
AATGGGCAGA CATTTGGTTA ATTGTGCCAG ATACCTAAAA TGTATGTTCA GAAAAGCATT 180
TTATCAACTC AGAAATATGA CTTATTTCTA GATTTCATGG CTTAATGAAT TTTTTCATTG 240
TTATATATAC CAAAGAGGCT TACGGGTTCA TTGATTGGTT TGAAAACCAG ACAGACGGCC 300
GTGAGCCACC ACGCCCAGCC AAGATGAACT CCTTAAGGAC AGGATTGGT AAGTGATTGA 360
CTTCTTTTTA GTTCCATGAT CTTGAGATTA TTTTtagctt TATAAATTTA GCAGTGGCAG 420
GGCCCGTGGA GAATCAGGTT AATGAGGTAA AGGCTTTCTG GGTATTTGCT GCCAAGGCCA 480
CATCACCAAT TTTCTCGATT TAAAAAACTG TCAAGAGATT TATTTTTCCTA TTGCAGGTTT 540
TAAAGTGGAG ATTCTGAAGT GGAAAATAGG TACTGTCAGA ACAAAGCTAC CTGGAAACAG 600
CATAGAGTGA AGCCTTTCGT GAGGGCTTGC AGGCCGCTGC TGAGTGGCAG TTTACAGAAG 660
AGGTCGCGGG GTGAGCCTCT TAGCAGGACA GAAAACAAGG CAGCAGCGCA CCTGCCACCC 720

CTTCACGAGC TGCTCCTTGA GCCTAAAAAG TAGGCTTTAT TCATCCCTTC TGTTCATTTA 780
CCAACCTGGG GGATTGATAC GACCGGGGAA AATGTTCTTA AACCAGGAAG CTGCGTTAGC 840
GAATCAGCTT TGGTAAGATC TCGCCAACAG CTAGCTGCTT AGGAGTACCC CCACGATACG 900
CACAGCACAC CACTGTCCCT TCACTGCACT TTCTTCCTGC CTTAGGTAGT TGGGCTTGCC 960
ACCCTAGTTT GCTTTTGTAG TGGTTTGCCA AGGTTAGAAG GCCTCGGCCC CCTCTGTCAT1020
GCTGGGAAGT GCCTACTCTC TGGGCCACTG CTGCAGAGGC CGTGGCACTT GTCATGGGTT1080
TGGAAGACCC AGCCATCTGC AGCAGAGGCA GCCTATCCCA TTGCAAGGAG AGGAACTGAA1140
CGGAGTAATT ATTCTACTCT TCTTTTACA TAAATGGTTT AATTTAAATA ATTCAAAATT1200
TGGAATTTCC TTTACAGAT ACTGATAATC CTTTCCAGTT CTTAAATAAA AACTGCACTT1260
GGATT
1265

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTTGGAGAGG CTGGTGGACA TAAAGAAAGG GAATACTCTG CTATTGCAGC ATCTGAAGAG 60
 GATCATCTCC GACCTGTGTA AACTCTATAA CCTCCCTCAG CATCCAGATG TGGAGATGCT 120
 GGATCAACCC TTGCCAGCAG AGCAGTGCAC ACAGGAAGAC GTGTCTTCAG AAGATGAAGA 180
 TGAGGAGATG CCTGAGGACA CAGAAGACTT AGATCACTAT GAAATGAAAG AGGAAGAGCC 240
 AGCTGAGGGC AAGAAATCTG AAGATGATGG CATTGGAAAA GAAAACTTGG CCATCCTAGA 300
 GAAAATTAAA AAGAACCAGA GGCAAGATTA CTTAAATGGT GCAGTGTCTG GCTCGGTGCA 360
 GGCCACTGAC CGGCTGATGA AGGAGCTCAG GGATATATAC CGATCACAGA GTTTCAAAGG 420
 CGGAAACTAT GCAGTCGAAC TCGTGAATGA CAGTCTGTAT GATTGGAATG TCAAACCTCT 480
 CAAAGTTGAC CAGGACAGCG CTTTGCACAA CGATCTCCAG ATCCTCAAAG AGAAAGAAGG 540
 AGCCGACTTC ATTCTACTTA ACTTTTCCTT TAAAGATAAC TTCCCTTTG ACCCACCATT 600
 TGTCAGGGTT GTGTCTCCAG TCCTCTCTGG AGGGTATGTT CTGGGCGGAG GGGCCATCTG 660
 CATGGAACCT CTCACCAAAC AGGGCTGGAG CAGTGCCTAC TCCATAGAGT CAGTGATCAT 720
 GCAGATCAGT GCCACACTGG TGAAGGGGAA AGCACGAGTG CAGTTTGGAG CCAACAAATC 780
 TCAATACAGT CTGACAAGAG CACAGCAGTC CTACAAGTCC TTGGTGCAGA TCCACGAAAA 840
 AAACGGCTGG TACACACCCC CAAAAGAAGA CGGCTAACCC TGGAGTATCA CCCTTCCTCC 900
 CTCCCCAGGC ACCACTGGAC CAATTACCTT TGAATGCTGT ATTTGGATCT CACGCTGCCT 960
 CTGTGGTTCC CTCCTCATTT TTTCTGGAC GTGATAGCTC TGCCTATTGC AGGACAATGA1020

 TGGCTATTCT AAACGCTAAG GAAAAAAAAC AAACACAGAA CTGTTTCAAG TACTCAAGAC1080
 TGAATTACAG ACCAACCAAC CACCTTGCTG GAACCCTTGC TAGCAGGCAT TCTTATAAAA1140
 GAAACTTTCG AGCCTCCTTA TATTGCTGGA AACTCAGCTG TGCTCCAGAC TAGAGCCTCC1200
 TTACCTATGC TATGGATTTT TAATTTATTT TCTCTTATTT CATGTACACT GCTTTTTTTT1260
 GTTACAGTGT ATGATGGATG TGTATGAAAA AAATGTATCT TTGGGAAAAA AATTACAGTT1320
 TGTTAATTTG 1330

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 762 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GGCGGCGGAG GAACCTCAGC AGCAGAAGCA    60
GGAGCCGCTG GGCAGCGACT CCGAAGGTGT TAACTGTCTG GCCTATGATG AAGCCATCAT    120
GGCTCAGCAG GACCGAATTC AGCAAGAGAT TGCTGTGCAG AACCTCTGG TGTCAGAGCG    180
GCTGGAGCTC TCGGTCCTAT ACAAGGAGTA TGCTGAAGAT GACAACATCT ATCAACAGAA    240
GATCAAGGAC CTCCACAAAA AGTACTCGTA CATCCGCAAG ACCAGGCCTG ACGGCAACTG    300
TTTCTATCGG GCTTTCGGAT TCTCCCACTT GGAGGCACTG CTGGATGACA GCAAGGAGTT    360
GCAGCGGTTC AAGGCTGTGT CTGCCAAGAG CAAGGAAGAC CTGGTGTCCC AGGGCTTCAC    420
TGAATTCACA ATTGAGGATT TCCACAACAC GTTCATGGAC CTGATTGAGC AGGTGGAGAA    480
GCAGACCTCT GTCGCCGACC TGCTGGCCTC CTTCAATGAC CAGAGCACCT CCGACTACCT    540
TGTGGTCTAC CTGCGGCTGC TCACCTCGGG CTACCTGCAG CGCGAGAGCA AGTTCTTCGA    600
GCACTTCATC GAGGGTGGAC GGACTGTCAA GGAGTTCTGC CAGCAGGAGG TGGAGCCCAT    660
GTGCAAGGAG AGCGACCACA TCCACATCAT TGCCTGGCC CAGGCCCTCA GCGTGTCCAT    720
CCAGGTGGAG TACATGGACC GCGGCGAGGG CGGCACCACC AA                          762

```

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1228 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

U.S. GOVERNMENT PRINTING OFFICE: 1980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

GAAAAGTTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT CTTTGTGTCC 60
TCCATTGGGA TCTATGTTTC TTCCACCTAC CCACCCGTGG CTGGGGCCAC TCTTTACTCA 120
GTGGCAATGT ACGGTGGATT AGTTCTTTTC AGCATGTTCC TTCTGTATGA TACCCAGAAA 180
GTAATCAAGC GTGCAGAAGT ATCACCAATG TATGGAGTTC AAAAATATGA TCCCATTAAAC 240
TCGATGCTGA GTATCTACAT GGATACATTA AATATATTTA TGCGAGTTGC AACTATGCTG 300
GCAACTGGAG GCAACAGAAA GAAATGAAGT GACTCAGCTT CTGGCTTCTC TGCTACATCA 360
AATATCTTGT TTAATGGGGC AGATATGCAT TAAATAGTTT GTACAAGCAG CTTTCGTTGA 420
AGTTTAGAAG ATAAGAAACA TGTCATCATA TTTAAATGTT CCGGTAATGT GATGCCTCAG 480
GTCTGCCTTT TTTTCTGGAG AATAAATGCA GTAATCCTCT CCCAAATAAG CACACACATT 540
TTCAATTCTC ATGTTTGAGT GATTTTAAAA TGTTTTGGTG AATGTGAAAA CTAAAGTTTG 600
TGTCATGAGA ATGTAAGTCT TTTTCTACT TTTAAATTTA GTAGGTTTAC TGAGTAACTA 660
AAATTTAGCA AACCTGTGTT TGCATATTTT TTTGGAGTGC AGAATATTGT AATTAATGTC 720
ATAAGTGATT TGGAGCTTTG GTAAAGGGAC CAGAGAGAAG GAGTCACCTG CAGTCTTTTG 780
TTTTTTTAAA TACTTAGAAC TTAGCACTTG TGTTATTGAT TAGTGAGGAG CCAGTAAGAA 840
ACATCTGGGT ATTTGGAAAC AAGTGGTCAT TGTTACATTC ATCTGCTGAA CTTAACAAAA 900
CTGTTTATCC TGAAACAGGC ACAGGTGATG CATCTCCTG CTGTTGCTTC TCAGTGCTCT 960
CTTTCCAATA TAGATGTGGT CATGTTTGAC TTGTACAGAA TGTTAATCAT ACAGAGAATC1020
CTTGATGGAA TTATATATGT GTGTTTTACT TTTGAATGTT ACAAAGGAA ATAACTTTAA1080
AACTATTCTC AAGAGAAAAT ATTCAAAGCA TGAAATATGT TGCTTTTTCC AGAATACAAA1140
CAGTATACTC ATGAAAAAAA AATGTTTTTT TATTTTGA TATTTATTGA ACTGTCTAAT1200
TGAATACAGC TTGCTCTTGT CACCTCAA 1228

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

GGCGGTGGTC CGCCATTTTCG TGGACGCCGG GTGAGTGAGA GAGTTGGTTG GTGTTGGGCC 60
GGAGGAAAGC GGGAAGACTC ATCGGAGCGT GTGGATTTGA GCCGCCGCAT TTTTAAACCC 120
TAGATCTCGA AATGCATCGT GATTCCTGTC CATTGGACTG TAAGGTTTAT GTAGGCAATC 180
TTGGAAACAA TGGCAACAAG ACGGAATTGG AACGGGCTTT TGGCTACTAT GGACCACTCC 240
GAAGTGTGTG GGTGCTAGA AACCCACCCG GCTTTGCTTT TGTGAATTT GAAGATCCCC 300
GAGATGCAGC TGATGCAGTC CGAGAGCTAG ATGGAAGAAC ACTATGTGGC TGCCGTGTAA 360
GAGTGGAACT GTCGAATGGT GAAAAAAGAA GTAGAAATCG TGGCCACCT CCCTCTGGG 420
GTCGTGCCCC TCGAGATGAT TATCGTAGGA GGAGTCCTCC ACCTCGTCGC AGATCTCCAA 480
GAAGGAGAAG CTTCTCTCGC AGCCGGAGCA GGTCCCTTTC TAGAGATAGG AGAAGAGAGA 540
GATCGCTGTC TCGGGAGAGA AATCACAAGC CGTCCCGATC CTTCTCTAGG TCTCGTAGTC 600
GATCTAGGTC AAATGAAAGG AAATAGAAGA CAGTTTGCAA GAGAAGTGGT GTACAGGAAA 660
TTACTTCATT TGACAGGAGT ATGTACAGAA AATTCAAGTT TTGTTTGAGA CTTCATAAGC 720
TTGGTGCATT TTTAAGATGT TTTAGCTGTT CAAATCTGTT TGTCTCTTGA AACAGTGACA 780
CAAAGGTGTA ATTCTCTATG GTTTGAAATG GATCATACGA GGCATGTAAT ACCAAGAATT 840
GTTACTTTAC AATGTTCCCT TAAGCCAAA TTGAATTTGC TTTGAACTTT TAGTTATGCA 900
CAGACTGATA ATAA 914

```

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

GAGGCAGCCC TGACACTATG CCACCTGCTG AGTCCTGGG TGTCACTAGA GAGCCTCACA 60
CTCTCCTACA ATGGCCTGGG CTCTAACATC TTCCGCCTGC TAGACAGCCT GCGGGCCCTG 120
TCAGGCCAGG CTGGATGTCG CCTCCGTGCC CTGCATCTCA GTGACCTGTT CTCACCACTG 180
CCCATCCTGG AGCTGACACG TGCTATCGTG CGAGCACTGC CCCTGCTACG GGTCCTCTCT 240
ATTCGTGTTG ACCACCCAAG CCAGCGGGAC AACCTGGTG TGCCAGGGAA TGCAGGGCCC 300
CCTAGCCACA TAATAGGCGA TGAGGAGATA CCAGAAAACCT GCCTGGAGCA GTTGGAGATG 360
GGNATTTCCA CGGGGAGCCC AGCCAGCCCC ACTGCTGTGC TCCGTTCTGA AGGCCTCGGG 420
TTCTCTGCAG CAGCTGTCCC TGGATAGTGC CACCTTTGCC TCTCCCAGG ATTTTGGGCT 480
TGTTTTGCAA ACACTCAAAG AGTACAACCT AGCCCTGAAA AGACTGAGCT TCCATGACAT 540
GAATCTCGCT GACTGTCAGA GCGAGGTGCT CTTTTTGCTA CAGAATCTGA CTCTGCAAGA 600
GATTACCTTC TCCTTCTGCC GTCTGTTTGA GAAGCGCCCA GCCCAATTC TGCCTGAGAT 660
GGTTGCTGCT ATGAAGGGCA ACTCCACACT GAAGGGCCTC CGGCTGCCAG GGAACCGCCT 720
GGGGAATGCT GGCCTGCTGG CCTTGGCAGA TGTTTTCTCA GAGGATTCAT CCTCCTCTCT 780
CTGTCAGCTG GACATCAGTT CCAACTGCAT CAAGCCAGAT GGGCTTCTGG AGTTCGCCAA 840
GCGGCTGGAG CGCTGGGGCC GTGGAGCCTT TGGTACCTG CGCCTCTTCC AAAACTGGCT 900
GGACCAGGAT GCAGTCACAG CCAGGGAAGC CATCCGGCGG CTCCGGGCTA CCTGCCATGT 960
GGTTAGCGAC TCATGGGACT CATCCCAGGC CTTGCGAGAT TATGTTAGCA CCATGTGATG1020
GGGCCCCGTAC CTCACAGTCT CATGCTCGGT ACCATCAGCT TGCAGGGGCT GAAGCATGGG1080
CTGCCCAGAA CCCCAACCAC CAGTTCTATC TTTCTCTTTC TGTGAC 1126

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 538 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

TAGACCACTG AGGAGACCAT AGAGCGGATG CTTTCATGCA CCCTTTACTG CACTTTCTGA    60
CCAGGAGCTA CTTTGAGTTT GGTGTTACTA GGATCAGGGT CAGTCTTTGG CTTATCAATA    120
AATTTTAATC TCTGTTAATC TTACCTGCTT TAAAAAAAAG TTCTTGTTGTG TTCGTATCTT    180

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TATTTATTCC CTAGTTTGCA GAACTGTCTG AATAAAGGAT ACAAGGATTA TTTCAATGTT    240
ACTGCACTGA AAAACGTGTA TGTATTAGTG TGCTAGATTA TTAGCAGAA TATTCACAAG    300
TTTCTGTTGA CTTGTTGAT TGAGCATGAC TACTAAATAT TATGTAATAA AAAGCATTG    360
TCATAACAGT CTTATGAAGT AGTTCTTCGA ATATAGAAAG TTCTATAATT TAGCCCATGA    420
AATGATAGGT TTTTAATTTT CAGAAATGGA GCTGCATGTA GAATGAGATC ACATGCTTTT    480
ATATGTGAAA TATTGGTTTT AGCAATTAAC AGAAGGCATA CTTTGCTAAT TTTATGGC    538

```

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 321 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

CCCTACAAC TGGTTGCAAAC TCAGGCTTTC CCCAGTGACC AACAAATTTTA ATTCCAAGAG    60
GTGAGGATCT CAGGAGGTGG CATTACCCCA CCAGGGAGCT AGGGAAAGGG AACCAAGCTG    120
TCTCCACACC CAGGAGAGGT GTCCCTCCAG CCAAGGCAGG CAGGACACTC TGCAGCTCTC    180
CCTCCTGTGC CCAGGCCCTT GACTACACTC TCATCTGCCA TCTGAGCTAA GCCAGGAAGG    240
CAGTTAAAGA AAGGCCCCCA AACATGAAGC AGGGACAAGG AGACGGACAG GGGTCAGATG    300
ACCCATTGAT AGGGAAGAGA G                                     321

```

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 847 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

AGACAAATCT TCTGCATGTC GGAGGAACGG GAATTATTCT GATGAAAAGA AAGATGCTAT 60
GTATTGGGAA AAAAGGCGGA AAAATAATGA AGCTGCCAAA AGATCTCGTG AGAAGCGTCG 120
EACTGAATGAC CTGGTTTTAG AGAACAACT AATTGCACTG GGAGAAGAAA ACGCCACTTT 180
AAAAGCTGAG CTGCTTTCAC TAAATTTAAA GTTTGGTTTA ATTAGCTCCA CAGCATATGC 240
TCAAGAGATT CAGAACTCA GTAATTCTAC AGCTGTGTAC TCAAGATT ACCAGACTTC 300
CAAATCCAAT GTGAGTTCAT TTGTGGACGA GCACGAACCC TCGATGGTGT CAAGTAGTTG 360
TATTTCTGTC ATTAAACACT CTCCACAAAG CTCGCTGTCC GATGTTTCAG AAGTGTCTTC 420
AGTAGAACAC ACGCAGGAGA GCTCTGTGCA GGAAGCTGC AGAAGTCCTG AAAACAAGTT 480
CCAGATTATC AAGCAAGAGC CGATGGAATT AGAGAGCTAC ACAAGGGAGC CAAGAGATGA 540
CCGAGGCTCT TACACAGCGT CCATCTATCA AAATATATG GGAATTCTT TCTCTGGGTA 600
CTCACACTCT CCCCCACTAC TGCAAGTCAA CCGATCCTCC AGCAACTCCC CGAGAACGTC 660
GGAAACTGAT GATGGTGTGG TAGGAAAGTC ATCTGATGGA GAAGACGAGC AACAGGTCCC 720
CAAGGGCCCC ATCCATTCTC CAGTTGAACT CAAGCATGTG CATGCAACTG TGGTTAAAGT 780
TCCAGAAAGT AATTCCTCTG CTTGCCACA CAAGCTCCGG ATCAAAGCCA AAGCCATGCA 840
GATCAAA

```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 573 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGAGGCTGCT	GGGGGCGGCG	CGTCCAGCTC	TGGGCCAGGG	GGTCCAAAGT	GCTCAGCCCC	60
CGGGGCACAG	CAGGACGTTT	GGGGGCCTTC	TTTCAGCAGG	GGACAGCCCG	ATTGGGGACA	120
ATGGCGTCTC	TTGGCCACAT	CTTGTTTTC	TGTGTGGGTC	TCCTCACCAT	GGCCAAGGCA	180
GAAAGTCCAA	AGGAACACGA	CCCGTTCACT	TACGACTACC	AGTCCCTGCA	GATCGGAGGC	240
CTCGTCATCG	CCGGGATCCT	CTTCATCCTG	GGCATCCTCA	TCGTGCTGAG	CAGAAGATGC	300
CGGTGCAAGT	TCAACCAGCA	GCAGAGGACT	GGGGAACCCG	ATGAAGAGGA	GGGAACTTTC	360
CGCAGCTCCA	TCCGCCGTCT	GTCCACCCGC	AGGCGGTTAG	AACACCTGGA	GCGATGGAAT	420
CCGGCCAGGA	CTCCCTGGC	ACCTGACATC	TCCCACGCTC	CACCTGCGCG	CCCACGGGCC	480
CCTCCGCCGC	CCCTTCCCCA	GCCCTGCCCC	CGCAGACTCC	CCCTGCCGCC	AAGACTTCCA	540
ATAAAACGTG	CGTTCCTCTC	GACAAAAAAA	AAA			573

(2) INFORMATION ON SEQ ID NO. 17:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 486 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

GCCGCACGGC TTGCTGGGGC TGGGCTCTTC CTCGCGGAAG TGGGGAGGAG GCGGTTGCGG 60
TTAGTGGACC GGGACCGGTA GGGGTGCTGT TGCCATCATG GCTGACCCCG ACCCCCGGTA 120
CCCTCGCTCC TCGATCGAGG ACGACTTCAA CTATGGCAGC AGCGTGGCCT CCGCCACCGT 180
GCACATCCGA ATGGCCTTTC TGAGAAAAGT CTACAGCATT CTTTCTCTGC AGGTTCTCTT 240
AACTACAGTG ACTTCAACAG TTTTTTTATA CTTTGAGTCT GTACGGACAT TTGTACATGA 300
GAGTCCTGCC TTAATTTTGC TGTTTGCCCT CGGATCTCTG GGTTTGATTT TTGCGTTGAC 360
TTTAAACAGA CATAAGTATC CCCTTAACCT GTACCTACTT TTTGGATTTA CGCTGTTGGA 420
AGCTCTGACT GTGGCAGTTG TTGTTACTTC TATGATGTAT ATATTATCTG CAAGCTTTCA 480
TACTGA 486

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 662 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

CTTTTTTCCT CTACTCCTTC CCCTTCACAC CCCCCTGGCT GGAAGGAACC TCGGCTTCCC 60
TGAAAGCTTG GGGGTCCCAC CCTTCTTACC CCACCCGGGA GGAACGCCCA GGGCCCCGGG 120
CTTGTTTCTC CTCTTGTTTT CCTTTTGGGC AGTTTGATCA CTGATCGAGT AAGGAATGAC 180
CTTTAGATTG TGC GACTTTT GTTTTTGTTT TTTTAAATTT TTTTAAACCA AGAATGATTT 240
CTCCTGCTTC CTTCTCCTCA CCATCTTCCC AGACGGAGTT CAAAGGCCAC TTCTCAAGCA 300
GCTTTTGGCA CCTTCAGCCT CAGAGTGGA TCTTTTAAAG ACAGGACCCC TATGTCCAGG 360
AAAGGGGAAA AGGAACCTTG CCAATGATAG TGACCACAGC AAAAGCAATA AAATAATAAA 420
ATAAAAAACA ATAGCACAGC CCTTGTTGAG GTCAGCAGGG AGGAGGGGCT GCCCGGAGTT 480
GGGTCCTTGC CTGGATTTTG ACACAGCAAC TTCCTGTAGT GAGCACTTTG TATGAATCGT 540
GGACTTCCTG TTCTCAAGGC GCAGGTATTT ATTCTGTATC TGTCTAGAGC ACACACCAAA 600
ATCCAACCTT CTAATAAACA TGATGGCGCA GTCCCAAAAA AGGAAACAGA AGAAGAAAAG 660
GG 662

```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATAGATTTTG	AGGGAAGGA	GAGAGGGAAG	GGTCAGGGTA	GAGACACCCC	TCCCTTGCCC	60
CTTTCCTGGG	CCCAGAAGTT	GGGGGGAGGG	AGGGAAGGA	TTTTTACATT	TTTTAACTG	120
CTATTTTCTG	AATGGAACAA	GCTGGGCCAA	GGGGCCCAGG	CCCTGTCCTC	TGTCCCTCAC	180
ACCCCTTTGC	TCCGTTTCATT	CATTCAAAAA	AACATTTCTT	GAGCACCTTC	TGTGCCCAGC	240
ATATGCTAGG	CCCACCAGCT	AAGTGTGTGT	GGGGGGTCTC	TACGCCAGCT	CATCAGTGCC	300
TCCTTGCCCA	TCCTTCACCG	GTGCCTTTGG	GGGATCTGTA	GGAGGTGGGA	CCTTCTGTGG	360
GGTTTGGGGA	TCTCCAGGAA	GCCCGACCAA	GCTGTCCCCT	TCCCCTGTGC	CAACCCATCT	420
CCTACAGCCC	CCTGCCTGAT	CCCCTGCTGG	CTGGGGGCAG	CTCCCAGGAT	ATCCTGCCTT	480
CCAACTGTTT	CTGAAGCCCC	TCCTCCTAAC	ATGGCGATTG	CGGAGGTCAA	GGCCTTGGGC	540
TCTCCCCAGG	GTCTAACGGT	TAAGGGGACC	CACATACCAG	TGCCAAGGGG	GATGTCAAGT	600
GGTGATGTCG	TTGTGCTCCC	CTCCCCCAGA	GCGGGTGGGC	GGGGGGTGAA	TATGGTTGGC	660
CTGCATCAGG	TGGCCTTCCC	ATTTAAGTGC	CTTCTCTGTG	ACTGAGAGCC	CTAGTGTGAT	720
GAGAACTAAA	GAGAAAGCCA	GACCCCTAAA				750

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

GGGGGAGAGA GGGAGGCCTT TGGGCGGTGG GGGCCACGGG GAGGGTGGTC CTCGGA CTAC 60
GTGCGGGACA GGAGGTCAGG GCTGGCAAGT CCCTCAGGCC TCCCTCGTTG CCCCAGCCTC 120
GCGGGCCGCC TAACTGCCCC GTTCCAAGGG TGCCACCGGA CCCCCTGGA GAGGAACTTC 180
TCCGTTGGCT GATTTCATCA CCACCCATTC CCGATTCCAC GTTTCCTTTA AGCGGGGCTG 240

GCGGAGCGCA AGGGGGCAAG GAACTGGATT GCGATTGGTC AGCACGTGCC TCGGTCGGCG 300
GTACAATTGG CTGAGGCGCT GGGCCTTGGG AAGCATTCCC CGACGGGATT GGTCTGCTCGCT 360
CTCGCAGAGC CCGCCTCCCG CAGTACAAGC GGCCCCCGGG TGGGGGGGGA GGAGGGGACT 420
GCGGGAGGAG GAACATGGCG GTGGCGGACC TCGCTCTCAT TCCTGATGTG GACATCGACT 480
GCGACGGCGT CTTCAAGTAT GTGCTGATCC GAGTCCACTC GGCTCCCCGC TCCGGGGCTC 540
GGGCTGCAGA GAGCAAGGAG ATCGTGCGCG GCTACAAGTG GGCTGAGTAC CATGCGGACA 600
CTACGACAA AGTGTCGGGC GACATGCAGA AGCAAGGCTG CGACTGTGAG TGTCTGGGCG 660
GCGGGCGCAT CTCCCACCAG AGTCAGGACA AGAAGATTCA CGTGTACGGC TATTCCATGG 720
CTATGGTCC TGCCCAGCAC GCCATTTCAA CTGAGAAAAT CAAAGCCAAG TACCCCGACT 780
ACGAGGTCAC CTGGGCTAAC GACGGCTACT GAGCACTCCC AGCCCGGGGC CTGCTGCCTC 840
CAGCAGCCAC TTCAGAGCCC CCGCCTTTGC CTGCACTCCT CTTGCAGGGC TGGCCCTGCC 900
TGCTCCTGCG GCAGCCTCTG GTGACGTGCT GTCCACCAGG CCTTGAGAC AGGCTAGCCT 960
GGCCACAGAA TTAAACGTGT TGCCACACCT GCCGGCTTCT G 1001

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 580 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

CGAAACGTGC GCAGGCGCCG GCCGCTGCGC TGCAGATGGC GGAAATGGAT CCGGTAGCCG 60
AGTTCCCCCA GCCTCCCGGT GCTGCGCGCT GGGCTGAGGC CCTTCTGCGA TGTTTTACCT 120
GGCTGCGGCT GTGTCAGATT TCTATGTTCC TGTCTCTGAA ATGCCTGAAC ACAAGATCCA 180
GTCATCTGGG GGCCCACTGC AGATAACAAT GAAGATGGTG CCAAAACTGC TTTCTCCTTT 240
GGTTAAAGAT TGGGCTCCCA AAGCATTTAT AATTTCTTTT AAGTTGGAGA CTGACCCCGC 300
CATTGTAATT AATCGAGCTC GGAAGGCTTT GGAAATTTAT CAGCATCAAG TGGTGGTGGC 360
TAATATCCTT GAGTCACGAC AGTCCTTTGT GTTTATTGTA ACCAAAGACT CGGAAACCAA 420
GTTATTGCTA TCAGAGGAAG AAATAGAAAA AGGCGTAGAG ATAGAAGAGA AGATAGTGGA 480
TAATCTTCAG TCTCGACACA CAGCTTTTAT AGGTGACAGA AACTGAAGTA AAAAGCCCTT 540
ATAGGATCAA AAATTGTTCA GGGCTCTTAG AGATGGTGAA 580

```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 740 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

GGATGCGTGG CGGGGAGCGC CGGGCTCTCC CGGAAGTCTC CCTGGACGGA AGTGGAAACG 60
GAAACCTTTT TAGGGAGTCC AAGGTACAGT CGCCGCGTGC GGAGTTGTTA CTGGTTACTT 120
GGCCTCATGG CGGTCCGAGC TTCGTTGAGG AACAACCTGTG AGATCGGCTG CTTTGCCAAG 180
CTCACCAACA CCTACTGTCT GGTAGCGATC GGAGGCTCAG AGAACTTCTA CAGTGTGTTC 240
GAGGGCGAGC TCTCCGATAC CATCCCCGTG GTGCACGCGT CTATCGCCGG CTGCCGCATC 300
ATCGGGCGCA TGTGTGTGGG GAACAGGCAC GGTCTCCTGG TACCCAACAA TACCACCGAC 360
CAGGAGCTGC AACACATTCG CAACAGCCTC CCAGACACAG TGCAGATTAG GCGGGTGGAG 420
GAGCGGCTCT CAGCCTTGGG CAATGTCAAC ACCTGCAATG ACTACGTGGC CTTGGTCCAC 480
CCAGACTTGG ACAGGGAGAC AGAAGAAATT CTGGCAGATG TGCTCAAGGT GGAAGTCTTC 540
AGACAGACAG TGGCCGACCA GGTGCTAGTA GGAAGCTACT GTGTCTTCAG CAATCAGGGA 600
GGGCTGGTGC ATCCAAGAC TTCAATTGAA GACCAGGATG AGTGTCTCTC TTTTCAAGTC 660
CCTTGTTGCG GGGATGTGAA CGAAGCATTA AGTGATTCTT GGGATGTGTA TAATGTGTCC 720
TTCGTGCCTG AAACCACCAG 740

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 975 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATGGGCTACA	ACCTGAGCCC	CCAGTTCACC	CAGCTTCTGG	TCTCCCGCTA	CTGCCCACGC	60
TCTGCCAATC	CTGCCATGCA	GCTTGACCGC	TTCATCCAGG	TGTGCACCCA	GCTGCAGGTG	120
CTGACAGAGG	CCTTCCGGGA	GAAGGACACA	GCTGTACAAG	GCAACATCCG	GCTCAGCTTC	180
GAGGACTTCG	TCACCATGAC	AGCTTCTCGG	ATGCTATGAC	CCAACCATCT	GTGGAGAGTG	240
GAGTGCACCA	GGGACCTTTC	CTGGCTTCTT	AGAGTGAGAG	AAGTATGTGG	ACATCTCTTC	300
TTTTTCCTGTC	CCTCTAGAAG	AACATTCTCC	CTTGCTTGAT	GCAACACTGT	TCCAAAAGAG	360
GGTGGAGAGT	CCTGCATCAT	AGCCACCAAA	TAGTGAGGAC	CGGGGCTGAG	GCCACACAGA	420
TAGGGGCCTG	ATGGAGGAGA	GGATAGAAGT	TGAATGTCCT	GATGGCCATG	AGCAGTTGAG	480
TGGCACAGCC	TGGCACCAGG	AGCAGGTCCT	TGTAATGGAG	TTAGTGTCCA	GTCAGCTGAG	540
CTCCACCCTG	ATGCCAGTGG	TGAGTGTTCA	TCGGCCTGTT	ACCGTTAGTA	CCTGTGTTCC	600
CTCACCAGGC	CATCCTGTCA	AACGAGCCCA	TTTTCTCCAA	AGTGGAATCT	GACCAAGCAT	660
GAGAGAGATC	TGTCTATGGG	ACCAGTGGCT	TGGATTCTGC	CACACCCATA	AATCCTTGTC	720
TGTAACTTC	TAGCTGCCTG	GGGCTGGCCC	TGCTCAGACA	AATCTGCTCC	CTGGGCATCT	780
TTGGCCAGGC	TTCTGCCCTC	TGCAGCTGGG	ACCCCTCACT	TGCCTGCCAT	GCTCTGCTCG	840
GCTTCAGTCT	CCAGGAGACA	GTGGTCACCT	CTCCCTGCCA	ATACTTTTTT	TAATTTGCAT	900
TTTTTTTCAT	TTGGGGCCAA	AAGTCCAGTG	AAATTGTAAG	CTTCAATAAA	AGGATGAAAC	960
TCTGGAAAAA	AAAAA					975

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAACACACAC	ACAGGTGTTT	TGACCAGCTC	AGGCTTGCCA	CAGTGAGCAA	CTCTGTGGCT	60
AGCAAAAGAG	AAGTTTATTT	GTGCCCAGCC	ATTGGTCACC	TTGGGTGATG	CACCAGATAG	120
CAGGCAGATG	TTGGTTCATT	GGCCTTCGTC	CTCTTTCCTC	CTAAAATAAT	ATTGGCTTTA	180
CCATCTTAAC	TCAGCTGTGG	GTTTTTTGTG	GGTTCCTGTT	TGTTTTTTGG	CATGAATTGT	240
CATCTTTGGT	GTTTTTTTAA	CCCCCAGCCC	CTCAAAAAAA	TAAGGCCTCC	AGGTATCAAG	300
ATCTCATATT	AGGATTTTCT	GTCCTTAATT	TTTTGAGCAA	AATCTGGAAA	ATGTGAAAGC	360
ATATTTAGAT	TTTATATACT	ATCTGAAATG	TGATTTGTTA	AGATTCTTAA	ATTTGGGCCT	420
CTTAGAATAA	TTTTGAATGA	GATCTACCGA	CTCACTTGTC	AGAATATTTT	TCACAGATTA	480
CTCTTTGGGCC	TTTTCATTAG	AAAGCTGTTT	GTTTGTCCTC	CTGTTGGTAC	ATTTGGTTAC	540
CTCATTTTGC	CGTTTCAGAT	TGTGAAAGCT	CACAGGGGTG	TTTTTTGGAA	TCATTTGCTG	600
AGTCATTTTC	TCAAATCATA	TTCCATTGTA	TCAGTTAACA	TATAGTTTTA	AATGTATGTA	660
TTATAAATAT	CTGTAACCAA	ATCATTGTA	GGCTTGATAA	ATTTTTAACA	AAGTTTGTAC	720
ATTTTTTATG	AAAGTTACTA	GTAATGCTTT	ACTAAGTAGT	GCAATGAATT	TTTATTTTAA	780
ATCCCTGTGC	CCAATTTTGG	AGTTGAGAGG	GTTGTTGGTA	ATAAATGTAT	GATGTACACT	840
TAAAAAATAA	AAAA					854

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 802 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTTTTTTCAG	AGTGCTAGGG	CTTTATTACA	AATGGAGTTG	ACTGCTAGAG	AGGCCCTTCT	60
CCAATCTTTC	TTCTGTACCT	TCTTCCCTCC	CAAAGACATC	CCTCTAGGGG	AGGTCAGTAG	120
GCCATTAGGT	AGGAGGAAAT	CTGGAGAGTG	AAAAGGGGCC	TTGCTTTTGT	CAAAGTCCTC	180
TGAAACAACC	ACTGAGTCTG	AAGGCTGGCT	CCAGTTGAGA	ATCTTCTAGT	GGAAGAGGTT	240
TAGCTCTCAT	CTTCAAGGTC	CTTCATTTCT	ACATCCTGGG	GGGCTTTTGT	CTTCTTTTGC	300
CTTTTGAGCT	GTGGTTCACT	AGTCCTGGCT	GGCTTTGAAG	GGGCTTCCAC	TTCCATGGCT	360
GTCTTCTCTT	TCTGGGCAAG	CCGGATCTGC	TGGAGGAGTT	TTCTGCGCTT	CTTCCCTGAC	420
AGTGTAATGT	TGGCACGTGC	ACTGGACGCC	CGCTTCTTGA	GGTGGTGCCG	CGTGATCAGC	480
CCTTGGTCTA	TCACAGCCCC	GACCACCCGG	TGCCTCAGAC	GCCGCTCCCG	ATTCAACACC	540
CGCCGGCGTT	TGAACAGCTT	CTTCTTCAGC	TCCGTTCCGG	GCCGTTTGAT	CTTCCCCCCC	600
GGAGCTCCCA	TAGTCGCGAT	TCCACTCCAG	TTCACGGTCC	GTACTTCCGC	TCAGCGCCGG	660
ATCCGCGGGC	TCCGCCCCGG	CCTTCCGCGG	GCCAATCGCA	ACTCGGGGGC	GGGTCTCTCG	720
GGTATATAAA	GGAGCTCCGC	GGTGCGGGAG	GCCTTTCGGA	GGGTGGTGAG	CTAGTAAGTG	780
TGGTTTTAGC	TGTAGTAGCC	AG				802

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 807 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

CCCCGTCCGC GCGTGGTGGC TGCTGCTGTG CATGTCCCTG CGATGGGAGT CTTGTGCCCCA    60
GCCTGTCACT TTCCTCCCCA GGGCAGAGCT CCCCTTCCTG CAAGAGTCTG GGAGGCGGGT    120
CAGGCTGTCC TGGCTGCTCT GGGGAAGCCG AGGGACAGCC ATAACACCCC CGGGACAGTA    180
GGTCTGGGCG GCACCACTGG GAACTCTGGA CTTGAGTGTG TTTGCCTCTT CCTTGGGTAT    240
GAATGTGTGA GTTCACCCAG AGGCCTGCTC TCCTCACACA TTGTGTGGTT TGGGGTTAAT    300
GATGGAGGGA GACACCTCCT CATAGACGGC AGGTGCCAC CTTTCAGGGA GTCTCCCAGC    360
ATGGGCGGAT GCCGGGCATG AGCTGCTGTA AACTATTTGT GGCTGTGCTG CTTGAGTGAC    420
GTCTCTGTCT TGTGGGTGCC AAGTGCTTGT GTAGAACTG TGTTCTGAGC CCCCTTTTCT    480
GGACACCAAC TGTGTCCTGT GAATGTATCG CTACTGTGAG CTGTTCCCGC CTAGCCAGGG    540
CCATGTCTTA GGTGCAGCTG TGCCACGGGT CAGCTGAGCC ACAGTCCCAG AACCAAGCTC    600
TCGGTGTCTC GGGCCACCAT CCGCCACCT CGGGCTGACC CCACCTCCTC CATGGACAGT    660
GTGAGCCCCG GGCCGTGCAT CCTGCTCAGT GTGGCGTCAG TGTCGGGGCT GAGCCCCCTG    720
AGCTGCTTCA GTGAATGTAC AGTGCCCGGC ACGAGCTGAA CCTCATGTGT TCCACTCCCA    780
ATAAAAGGTT GACAGGGAAA AAAAAAA                                     807

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(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 777 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

CTCTCTGCCA GCTGATGTGC CCTGTTGCCC CCCACCCCAT CCCGCACAGA ACCATCCCTG 60
CATTCCACAG GGGACTCGGG CAAGGGTGCC GAAGATAGAC AAGAGGCACA CAGAGACAGA 120
CCAAGTGGCA GCCAGGCAGC CCCAGAGGAG AGAGACATTC AGACAGAGGA AAGTCTCCCT 180
GCCCCTCATT CCTTCCAAGA TGAGAAAAAC TTGCCGCCAC CCCCCGACAC TGATGCCAGG 240
GAGGTGGGAG GAAGAAGTGG GAAATTTCCC TTCCCAGTAC CCCCAGAAGC GTCTGAGCCT 300
TCAATGTTGA ATTTTTTCTT TATTAAAATT ACTTTTATCT TATAAAATCA ACTAATCAAA 360
AATGATATAG ACGACAGCAC TGGCTCTGTG AAGGTGGCAT CTTTCTGGGC AGGCAGGCCA 420
TGGGGCATGG AGGAGGGTGC AAAGATATGG GTTGCTGTCT TCTGGCCTCC AGCTGCATGG 480
AGGCCGGCCC AGGGTCTAGG GTGTGCACTG GGCAAGGGCA GGGCGGCAGG TGTCAGGCCG 540
GCTTGACAA TGAAACCCTG ACCTTGCTGC ATTCCTTTTG CTTCCACCAC CACTAGCTTC 600
TTTGAATCT TGGGGTGGGG GTCATCTTTG GGGATTATGG CTGCCACCCG GGATTTGAGT 660
GTAGGGAGTG TGGGAGCAGC CTTGGCAGAT GGGGCACCCG TGCCCTGCAG GTGTTGACAA 720
GATCCGCCAT CTGTAATGTC CTTGGCACA TAAACCAAA TGTCAGTTTC AAAAAAA 777

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(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 501 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

CCGATTCCG CCCC GCCCGC TCGATCCGG TTCCGCTCCC CACAACCCGC TCTGTGGCGG 60
GGCTTCCGGT CGGGAGGGTC CGCCAGCTCT CGCGTCCTTT GCTGGGTCCA GACACCGGTT 120
CCGTTGCAAA CATTTT TAAA GGGCTGGTTA TTCTTCCTGA AATGAGTTTG GTGATTAGAA 180
ATCTGCAGCG AGTCATCCCC ATCAGGAGAG CGCCACTTCG CAGTAAGATC GAGATTGTAA 240
GGAGGATTTT AGGAGTGCAG AAATTTGACC TGGGGATCAT CTGTGTTGAC AACAAGAATA 300
TTCAGCACAT TAATAGAATC TACAGAGATA GAAATGTCCC AACCGATGTG CTTTCTTTTC 360
CATTTTCATGA GCATCTGAAA GCAGGTGAAT TTCCCCAGCC TGATTTTCCA GATGACTACA 420
ATTTGGGAGA CATTTTCCTA GGAGTGGAGT ATATCTTCCA TCAGTGTAGA GAAGATGAAG 480
ATTACAATGA CGTCCTGACT G

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ATTTTGACCC TAAACTTTTG GAAGGAAAAG TAAAGGAGGA TCCTGACCAG GGGGAATCCA 60
TGAAACCTTT AACCTTTGCA AGGTTCTACT TGCCAATTCT GGTTCCCAGC GCAAAGAAGG 120
CCATATACAT GGATGATGAT GTAATTGTGC AAGGTGATAT TCTTGCCCTT TACAATACAG 180
CACTGAAGCC AGGACATGCA GCTGCATTTT CAGAAGATTG TGATTTCAGC TCTACTAAAG 240
TTGTCATCCG TGGAGCAGGA AACCAGTACA ATTACATTGG CTATCTTGAC TATAAAAAGG 300
AAAGAATTCG TAAGCTTTCC ATGAAAGCCA GCACTTGCTC ATTTAATCCT GGAGTTTTTG 360
TTGCAAACCT GACGGAATGG AAACGACAGA ATATAACTAA CCAACTGGAA AAATGGATGA 420
AACTCAATGT AGAAGAGGGA CTGTATAGCA GAACCTGGC TGGTAGCATC ACAACACCTC 480
CTCTGCTTAT CGTATTTTAT CAACAGCACT CTACCATCGA TCCTATGTGG AATGTCCGCC 540
ACCTTGGTTC CAGTGCTGGA AAACGATATT CACCTCAGTT TGTAAGGCT GCCAAGTTAC 600
TCCATTGGAA TGGACATTTG AAGCCATGGG GAAGGACTGC TTCATATACT GATGTTTGGG 660
AAAAATGGTA TATTCCAGAC CCAACAGGCA AATTCAACCT AATCCGAAGA TATACCGAGA 720
TCTCAAACAT AAAGTGAAAC AGAATTTGAA CTGTAAGCAA GCATTTCTCA GGAAGTCCTG 780

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GAAGATAGCA TGCCTGGGAA GTAACAGTTG CTAGGCTTCA ATGCCTATCG GTAGCAAGCC 840
ATGGAAAAAG ATGTGTCAGC TAGGTAAAGA TGACAACTG CCCTGTCTGG CAGTCAGCTT 900
CCCAGACAGA CTATAGACTA TAAATATGTC TCCATCTGCC TTACCAAGTG TTTTCTTACT 960
ACAATGCTGA ATGACTGGAA AGAAGAACTG ATATGGCTAG TTCAGCTAGC TGGTACAGAT1020
AATTCAAAAC TGCTGTTGGT TTTAATTTTG TAACCTGTGG CCTGATCTGT AAATAAACT1080
TACATTTTTC AAAAAAAAAA AAAA

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1104

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 810 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GCCATCCTTT	ATCATCCACA	GCAATCCCAT	CTGGTTGGGA	GCACTGCTCT	GGGTCTCACA	60
CTGCCCCCTCC	TCTATCCTAG	GGAGCCTGAG	GCCCAGGGGT	GGAAAGATCC	AGTTGCGGGT	120
GGGGGGTAGT	GAACCGTGCA	GGATAATGAA	AGCAACTTGC	TTTGGAATG	ACCTACCGCT	180
ACCCGTTGTC	TGAGACTGAG	ATTATCTCAG	ACTGTCTTCT	GGCTTCTGCC	AAAACACTCC	240
CTTAACAGAA	AGCACCGAGG	GGATGGGGGT	AGGGGGGTTG	GGGAGAGTGA	GGCTTGAGTG	300
TGAAGGAAGT	CTCATATATG	CAGAGCTGAA	ATCTCCCTCT	TTGTATGTCC	ACACTTTTGT	360
CTTGTTCTCT	AGACTGATTC	TTGCTATTCC	AAATCCTCTT	CCACGTTGAC	AGCCCTTCAG	420
ATATTTCAAC	ACTCCTCTCA	GCATCCTCCA	CTTCCCCCAT	CTCTCCAAGC	TGAACTTGGT	480
TCACAGGGTG	GGATTGTGTA	TGTGCATGCA	GGAGGTGGGG	GTGGACAGTG	CCCTGGGCTG	540
GAATCCCCCT	TAGTTCTAAG	TGCCTCCTTG	CCCGCAGCTT	CGAGAGCTGT	GCCCAGGAGT	600
GAACAACCAG	CCCTACCTCT	GTGAGAGTGG	TCACTGCTGC	GGGGAGACTG	GCTGCTGCAC	660
CTACTACTAT	GAGCTCTGGT	GGTTCTGGCT	GCTCTGGACT	GTCCTCATCC	TCTTTAGCTG	720
CTGTTGCGCC	TTCCGCCACC	GACGAGCTAA	ACTCAGGCTG	CAACAACAGC	AGCGGCACGT	780
GGAAATCAAC	TTGTTGGCCT	ATCATGGGGC				810

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 826 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TGGAAATCAT	GGCAACTACA	CAGGATGTTG	CTTACCAGGA	CGGAGTTTTG	GTATCTTAGT	60
ACTGAAGTTA	GCACTATGTT	TACATGCAAA	AGATTAAGGA	AAAAACCCTT	AAAGTGGACA	120
GGTATCCAAA	GTTTCATTTTC	TGTGACTCAT	CAAAGTGACA	AAAGACTTGT	AACAACTTTG	180
CCTGGACTTT	TTTCATTTTA	CAACAGTTCA	TCCATTACACA	ATGATTTTGT	TCTCTGCTCC	240
ATATTTTTTA	ATCCCTTAAG	CATTTGATGA	AACACTCTTT	AGTGCTATAT	GCATTTTCTT	300
ACTTTTGTTA	AAAATGTGAC	AATTGTCAAA	AAATGCACTA	AAATGTAAAT	GGAGATTGAA	360
CAAGTTCACT	TTCCAGCTTA	TAGGCAACTT	TATACAGACT	TGAACATTTT	CTCCAGTTGT	420
TTAGTAAAAG	TGAAAGAGAA	AGGGTTTTTC	CTGCCACAGG	ATATAACTTT	TTTTTATATA	480
ACAAGCATAA	CACACCACTG	CTTTTGGTGG	AAAAGTGCAG	AATAGTATGT	ACCTTTTATG	540
AAGAAAAATG	TAATTTACAA	TATTCAGTGA	GAATGTTACT	GCTGATTTTC	TTTCCAAGG	600
TGTAGAATAT	TCTTTGATTT	ATAGAATTCA	TTTTTGACCC	AGATGATGGT	TCCTTTACAG	660
AACAATAAAA	TGGCTGAACA	TTTTCACAAA	TAGAGTGTA	CGAAGTCTGG	ATTTCTGATA	720
CCTTGTCATT	TGGGGGATTT	TATTTTACTT	TGTTGCTTTA	AAATTCAATG	CAGAGAAGTT	780
GTTGACTGTA	GGGGAAATAA	AGTTAATTCA	AATTTTGAAA	AAAAAA		826

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 578 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTTCTTAACT	GTTCCATTTT	CCGTATCTGC	TTCGGGCTTC	CACCTCATTT	TTTTCGCTTT	60
GGCCATTCTG	TTTCAGCCAG	TCGCCAAGAA	TCATGAAAGT	CGCCAGTGGC	AGCACCGCCA	120
CCGCCGCCGC	GGGCCCCAGC	TGCGCGCTGA	AGGCCGGCAA	GACAGCGAGC	GGTGCGGGCG	180
AGGTGGTGCG	CTGTCTGTCT	GAGCAGAGCG	TGGCCATCTC	GCGCTGCGCC	GGGGGCGCCG	240
GGGCGCGCCT	GCCTGCCCTG	CTGGACGAGC	AGCAGGTAAA	CGTGCTGCTC	TACGACATGA	300
ACGGCTGTTA	CTCACGCCTC	AAGGAGCTGG	TGCCCCACCT	GCCCCAGAAC	CGCAAGGTGA	360
GCAAGGTGGA	GATTCTCCAG	CACGTCATCG	ACTACATCAG	GGACCTTCAG	TTGGAGCTGA	420
ACTCGGAATC	CGAAGTTGGA	ACCCCCGGGG	GCCGAGGGCT	GCCGGTCCGG	GCTCCGCTCA	480
GCACCCTCAA	CGGCGAGATC	AGCGCCCTGA	CGGCCGAGGC	GGCATGCGTT	CCTGCGGACG	540
ATCGCATCTT	GTGTCGCTGA	AGGCCTCCCC	CAGGGACC			578

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 799 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGCTTTTGT	CACACTTTAA	ATAGCAGTCC	CAGAATGATT	TCACTACAGA	CTCTCTGGAA	60
AGCCTGGGAG	CTGAATTCCG	GAAGATCCCC	ACATCGATGA	AAGCAAAGCG	AAGCACCAAG	120
CCATCATCAT	GTCCACGTCG	CTACGAGTCA	GCCCATCCAT	CCATGGCTAC	CACTTCGACA	180
CAGCCTCTCG	TAAGAAAGCC	GTGGGCAACA	TCTTTGAAAA	CACAGACCAA	GAATCACTAG	240
AAAGGCTCTT	CAGAAACTCT	GGAGACAAGA	AAGCAGAGGA	GAGAGCCAAG	ATCATTTTTG	300
CCATAGATCA	AGATGTGGAG	GAGAAAACGC	GTGCCCTGAT	GGCCTTGAAG	AAGAGGACAA	360
AAGACAAGCT	TTTCCAGTTT	CTGAAACTGC	GGAAATATTC	CATCAAAGTT	CACTGAAGAG	420
AAGAGGATGG	ATAAGGACGT	TATCCAAGAA	TGGACATTCA	AAGACCAAGT	GAGTTTGTGA	480
GATTCTAACA	GATGCAGCAT	TTTGCTGCTA	CCTTACAAGC	TTCTCTTCTG	TCAGGACTCC	540
AGAGGCTGGA	AAGGGACCGG	GACTGGAAAG	GGACCAGGAC	TGAACAGACT	GGTTACAAAG	600
ACTCCAAACA	ATTTTCATGCC	CTGTGCTGTT	ACAGAGGAGA	ACAAAATGCT	TTCAGCAAGG	660
ATTTGAAAAC	TCTTCCGTCC	CTGCAGGAAA	GGATTGACGC	TGATAGAAGA	GCCTGGACAG	720
ATGTAATGAG	AACTAAAGAA	AACGATGGCT	GGAGATGACA	TTTATCCAGG	GTCACCTTGT	780
CAGGCCCTAG	GACTTAAAT					799

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

AATTTATTTT TTTTTCATGG TCTGTCAGGT TTTATTTATA GAGTCTGGTG AACTTGA ACT 60
AGAGAAAGCT GCAAAAAGTG GTTTGGAGAG CATGGCAGGG CCATGGAGAA GGGCTAATAG 120
AAGCAGGTCC CTTGCCCAGA CCCTCAGGGA GCCCTTTTGG TGGATAGCGG ACACCTGAGG 180
CAGGAGGTGG CAGGGGCCAA GTCCAGGCAG GCAGCAGCAG GGCTGCAACT GAGAGCTGAG 240
GCTGGAGAGG TAGCGCTCGC CCTAACCTGA TCCTGCAGGT CTCAGGCCCT GGGGTCATAT 300
ACTCGCCCCA TGAAGACAGG GAACTTGTGC TGCTGGTCCC AGAGCACGAA GAGGAAGGGC 360
TGCTGCACTT CAAAGACCAG CAGGGTGCGG GCCACAGAGA TGGCGGAGGC TGCAGCCGCC 420
TCCACCCAG TCTCTGTCAG TTCCAGCACT GTCTGGTGCT GCATCGCAGA AACCTGAAGA 480
TCTGGGTCCT CTGTCAGCCC ACACAGGTTA AGGTCATAAG AAAAATCGAA GAATTCCAAT 540
TTCTCCATGA TTGAGAGCAT ATCCTGGCTG GTCGTCACCT TGATGCGGGG TAGTGTTAGG 600
AGAGTGGGCT GGAACCTTGA CATCTCCAGT TTCTCCATGA TGGCCTTGAA AACAGAAGGG 660
CTGAGAGCCT GTTCCATGTC TTCAAGACGA TGTTTCAGGT TCTGGGGTAC CAGGATCACC 720
AAACTCAGAT TGTGGGAGAG CTGCAGCTGC CCCACCTTGG CTTTCAAAGT TTGGTCAATG 780
AAATGGGCCA CAGGGTACTT CTTGCTATTC ATCATGGGCA CTTTTATAAC TGAGTTTTTG 840
AAGTGAAAGG GTTCCATTCT GGTTTTCTTG GGATCAAATG TTGTCTTCCA CTTGGCACTC 900
AGGTAGATAG CATTGAGGAG GACAAGGCGG GTATCGGAGG GCAGACTGTC TAGCAGCCGG 960
CTGATCTTGT TGTGGGTGTT CTTGGCCACC CAGGTGTTGA TGAGCTCCAA AGTTGAATAG1020
CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG AAAGCCAAGG TGGGGCAGCT1080
GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC CAGAACCTGA AACATCGTCT1140
TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG GCCATCATGG AGAAACTGGA1200

GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC ATCAAAGTGA CGACCAGCCA1260
GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT TTTTCTTATG ACCTTAACCT1320
GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG ATGCAGCACC AGACAGTGCT1380
GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC GCCATCTCTG TGGCCCGCAC1440
CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG CTCTGGGACC AGCAGCACAA1500
GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC TGAGACCTGC AGGATCAGGT1560
TAGGGCGAGC GCTACCTCTC CAGCCTCAG TCTTCAGTTG CAGCCCTGCT GCTGCCTGCC1620
TGGAATTGGC CCCTGCCACC TCCTGCCTCA GGTGTCCGCT ATCCACCAA AGGGCTCCCT1680
GAGGGTCTGG GGCAAGGGAC CGTGCTTCTA ATTAAGCCCT TCTTCCAATG GGCCTTGCA1740
GGC

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1743

(2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

GCCAATCGAA TCGTCCTGGG AGGCTTTTCA CAGGGCGGGG CCCTGTCCCT CTACACGGCC 60
CTCACCTGCC CCCACCCTCT GGCTGGCATC GTGGCGTTGA GCTGCTGGCT GCCTCTGCAC 120
CGGGCCTTCC CCCAGGCAGC TAATGGCAGT GCCAAGGACC TGGCCATACT CCAGTGCCAT 180
GGGGAGCTGG ACCCATGGT GCCCGTACGG TTTGGGGCCC TGACGGCTGA GAAGCTCCGG 240
TCTGTTGTCA CACCTGCCAG GGTCCAGTTC AAGACATACC CGGGTGTCAT GCACAGCTCC 300
TGTCTCAGG AGATGGCAGC TGTGAAGGAA TTTCTTGAGA AGCTGCTGCC TCCTGTCTAA 360
CTAGTCGCTG GCCCCAGTGC AGTACCCAG CTCATGGGGG ACTCAGCAAG CAAGCGTGGC 420
ACCATCTTGG ATCTGAGCCG GTCGAGCCCC TGTCCCCACC CTTCTGACC TGTCTTTTC 480
CCACAGGCCT CTGGGGGCAG GTGGCAAGGC CTGGCCGGGC CTTCTTCCT GGCCTTAGCC 540
ACCTGGCTCT GTCTGCAGCA GGGGCAGGCT GCTTTCTTAT CCATTTCCCT GGAGGCGGGC 600
CCCCCTGGCA GCAGTATTGG AGGGGCTACA GGCAGCTGGA GAAAGGGGCC CAGCCGCTGA 660
CCCACTCACT CAGGACCTCA CTCACTAGCC CCGCTTTGGG CCCCCTCCTG TGACCTCAGG 720
GTTTGGCCCA TGGGGCCCTC CCAGGCCCTT GCCCCAACTG ATTCTGCCCA GATAATCGTG 780
TCTCTGCCT CCACTCAGCT GCTTCTCAGT CATGAATGTG GCCATGGCCC CGGGGTCCCC 840
TTGCTGCTGT GGGCTCCCTG TCCCTGGGCA GGAGTGCTGG TGAGGAGGTG GAGCCTTTTG 900
AGGGGGGCCT TCCCTCAGCT GTTTCCCCAC ACTGGGGGGC TGGGCCCTGC CTCCCCGTTA 960
CCCTCCTTCC CTGCAGGCCT GGAGCCTGTA GGGCTGGACT GAGGTTTCAG TCTCCCCCA1020

GCTGTCTCAC CCCCACCTTG TCCCCACTCT AGAGCAGGGA GGCAGTGGGG GAGGAGTTGT1080
GTCTCGTCTT CTGTCTCCAT GTGGTTTTTG GGTGTTTTTC TTGTTGTGTC CTGGATTCCG1140
ATAAAATTAA AGAAATTGCT TCCTCAAAAA AAAAAAAAAA AAA
1183

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(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GTTTTTTTTT	TTACTGCAGA	AAATTGGTGG	TATTTTCACA	TTCATAGTGT	TTCTATCCAA	60
TTTCAGTACC	CACATTTAAT	GAGGAAAAAA	TGTTTTACCA	ATGAAGGAGG	AATTCTTAAA	120
TTAGCTGTAA	TGTTAGGTTG	GAGAAAAATT	GGTATTTAGG	GTATTTTCAA	GGTACCATCA	180
AATCAGATTT	CTGTTTTTTT	GTAAAAAA	ATTTTTTTAA	TCAGTATTGT	TTTTACAAGT	240
AATATACTTT	GAAACTCTTG	AACTAATAGT	CTCAAAAAC	CTAGAGGACA	GTCTGAGAAC	300
ACGTATTTCT	ATTGTTCTAA	ATAAATACAT	GTTTTTGAAT	AGTTCAATCA	TGAATTATTG	360
ACTATGTCTT	CATCAAAAGT	GTAAATCCCT	CTCAGGTCT	CTGGTGAAGA	CCTTCAAGAG	420
TTTGGTTTTT	TCTCCCAGGA	AATTGGAAGG	TAGAATTGTA	AATTCATAGA	ACTTCTTTTA	480
TAATGGTGTA	CCTCAGCAGC	TGCCTTTCAA	TTTATGCCAA	GTCCTTACAG	AGTTTATACT	540
TGAATAGTAA	ATATGTCTTC	TGAGTTTTAC	AGTGTCTTAA	ACTCAATGCA	CATTTTTTTT	600
TCTTCTTTTT	CCACCCCTTC	TTGTTTGTAG	TTCATTATAC	CTGTCCTATT	ACAGAACTGA	660
TTTCCTTCCT	GGCTGTACAT	GTTGGGGTGC	TGGATTTTTT	TCCGTGTCTT	TAGTCTTCGG	720
ATACATGTTC	TCTTCTTTAG	CTTGTGGTGA	ATACAGTAAT	TTGCATTG		768

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

CCCTGCTGTG AAGTCCTGGC AGGTGTTGGT AATGTGTGGA AATGCAGTCA GCAAGTTTGC 60
TGGGGAGTTT GATAAAAGTA TAAAACAAAA CAAAAAAGC CTCGGTATAA TTTTGTTCCTA 120
CGACTTCTTC TGTAGCTTTA CACCAGAAGG AAGGAATGGG CTACAGCAGG TAGTGGAGGA 180
AGAGGGGGGT GAGCAGGTGT ATTAAAATAG CTTACGGGTA AGGCCTAAAA GGTCACCCCT 240
CGGCCCCCTC TCCAAAAGAA GGGCATGGGC ACCCCCAGGA GAGGATGGCC CCAAAAACCT 300
TATTTTTTATA CATGAGAGTA AATAAACATA TTTTTTTTAC AAAAATAACT TCTGAATTTA 360
TCAGTGTTTT GCCGTAAAAA ATATTCCTCT ATAGTAAATT ATTTATTGGA AGATGACTTT 420
TTTAAAGCTG CCGTTTGCCT TGGCTTGGTT TCATACACTG ATTTATTTTT CTATGCCAGG 480
CAGTAGAGTC TCTCTGCCTC TGAGGAGCAG GCTACCCGCA TCCCACTCAG CCCCTCCCTA 540
CCCCTCAAGA TTTGATGAAA ATTCCAACCA TGAGGATGGG TGCATCGGGG AAGGGTGAGA 600
AGGAGAGCCT GCCTGCTCAG GGATCCAGGC TCGTAGAGTC ACTCCCTGCC CGTCTCCCAG 660
AGATGCTTCA CCAGCACCTG CCTCTGAGAC CTCGCTCTCT GTTCCAGCAA CCCTGGTTGG 720
GGGGTCAGAC TTGATACACT TTCAGGTTGG GAGTGGACCC ACCCCAGGGC CTGCTGAGGA 780
CAGAGCAGCC AGGCCGTCCT GGCTCACTTT GCAGTTGGCA CTGGGTTGGG GAGGAAGAGA 840
GCTGATGAGT GTGGCTTCCC TGAGCTGGGG TTTCCCTGCT TGTCCAGTTG TGAGCTGTCC 900
TCGGTGTTAC CGAGGCTGTG CCTAGAGAGT GGAGATTTT GATGAAAGGT GTGCTCGCTC 960
TCTGCGTTCT ATCTTCTCTC TCCTCCTTGT TCCTGCAAAC CACAAGATAA AGGTAGTGGT 1020
GTGTCTCGA                                     1029

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(2) INFORMATION ON SEQ ID NO. 44:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 736 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ATTCTCTGGGT TGAAATATTT TGTAGGGATT GCTTATTATA TTATTTTAGC TGATGAACCT 60
CAGGACAACG GCTACAGACA CACACATACA TACACGCACA CAAAATCTCA GCTGTTGAAG 120
AGTGGGCTTG GAATCAGACT TCTGTGTCCA GTAAAAAACT CCTGCACTGA AGTCATTGTG 180
ACTTGAGTAG TTACAGACTG ATTCCAGTGA ACTTGATCTA ATTTCTTTTG ATCTAATGAA 240
TGTGTCTGCT TACCTTGTTT CCTTTTAATT GATAAGCTCC AAGTAGTTGC TAATTTTTTG 300
ACAACTTTAA ATGAGTTTCA TTCACTTCTT TTAATTAATG TTTTAAGTAT AGTACCAATA 360
ATTTTCATTAA CCTGTTCTCA AGTGGTTTAG CTACCATTCT GCCATTTTTA ATTTTATTT 420
AATTTTATTT GCTTGAGCAC ACTGATCAAC CACTGAACTG CCTTCTTCCA TTGTCCTGCA 480
ATGATATAAG GGTTACATTT TTGTGTATAT GGCTTTCATA GTTGGGATTT CAGAGCACTG 540
ATACCAGATA TTTTCAGTTT GTTCTCTGGG GGAATTTTCAT TTGCATCTAT GTTTTGTAGCT 600
ATCTGTGATA ACTTGTTAAA TATTAAAAAG ATATTTTGCT TCTATTGGAA CATTTGTATA 660
CTCGCAACTA TATTTCTGTA AACAGCTGCA GTCAAAAATA AAACACTGAA AGTTTTTCATT 720
TTGCAGTGGA AAAAAA
736

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(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGACCGTGTG TCGGCCGTGG CGCTGCCCAA GCTGCCCATC TCGCTCACCA ACACCGACCT 60
 CAAGGTGGCC AGCGACACAC AGTTCTACCC TGGCCTCGGG CTGGCCCTGG CCTTCCACGA 120
 CGGCAGCGTC CACATCGTGC ACCGGCTCTC ACTGCAGACC ATGGCCGTCT TCTACAGCTC 180
 CGCGGCCCCG AGGCCTGTGG ATGAGCCGGC CATGAAGCGC CCCCGCACCG CGGGCCCCGC 240

CGTCCACTTA AAGGCTATGC AGCTATCGTG GACGTCACCTG GCCCTGGTGG GGATTGACAG 300
 CCACGGGAAG CTGAGCGTGC TCCGCCTCTC ACCTTCCATG GGCCACCCGC TGGAGGTGGG 360
 GCTGGCGCTG CGGCACCTGC TCTTCCTGCT GGAGTACTGC ATGGTGACCG GCTACGACTG 420
 GTGGGACATC CTGCTGCACG TGCAGCCCAG TATGGTACAG AGCCTGGTGG AGAAGCTGCA 480
 CGAGGAGTAC ACGCGCCAGA CCGCTGCCCT GCAGCAGGTC CTCTCCACCC GGATCCTGGC 540
 CATGAAGGCC TCGCTCTGCA AGCTGTGCGC CTGCACGGTG ACCCGCGTGT GCGACTACCA 600
 CACCAAGCTC TTCCTCATCG CCATCAGCTC CACCCTGAAG TCGCTGCTGC GCCCCCACTT 660
 TCTCAACACG CCTGACAAGA GCCCCGGCGA CCGCTGACC GAGATCTGCA CCAAGATCAC 720
 CGACGTCGAC ATTGACAAGG TCATGATCAA CCTCAAGACG GAGGAATTTG TGCTGGACAT 780
 GAACACACTG CAGGGCGCTG CAGCAGCTCT TGCAGTGGGT GGGCGACTTC GTGCTGTACC 840
 TGCTGGCCAG CCTACCCAAC CAGGGTTCCC TGCTGAGGCC GGGCCACAGC TTTCTGCGGG 900
 ACGGCACCTC GCTGGGCATG CTTGCGGAAT TGATGGTGGT CATCCGCATC TGGGGCCTTC 960
 TGAAGCCCAG CTGCCTGCCC GTGTATACGG CCACCTCGGA TACCCAGGAC AGCATGTCCC1020
 TGCTCTTCCG CCTGCTCACC AAGCTCTGGA TCTGCTGTGC CGATGAGGGC CCAGCGAGCG1080
 AGCCGGACGA GCGCTGGTG GATGAATGCT GCCTGCTGCC CAGCCAGCTG CTTATCCCCA1140
 GCCTGGACTG GCTGCCAGC 1159

(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 690 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AGAGCGGCCG CCCCTCTTTT TTTCTCTTTC TTTTTTTTTT TTTTGCATA TCAGAAATGC   60
ATTTTAATTT TTATTTGAAA ACAACTTAAA TTTTtagaca AATGATTTTA GTATATAAAT  120
TTGCTTTTGT TTTTATACAG AATATAAAGA TTTCCCTCAT TAATCTTCCA TGTGAAGGGT  180
ATTACAAGCC TGGAGGAAGA TACTTTCTGC ACACAAGTAT GTATCTTATG TGTGCAGTAT  240
TGGAAACCAA TGGTGTAGTG CTCCTACACA TAAATGGGGT CAAGTGACAT CACAAATTAA  300
AAGGGGGAAA GAGAAATATT CTAGTTAATC AGATGCAAGA AGCAAACAAG ACGCAAAAAC  360
TGTGCAATA AGACCAAGCC AGTAACTTTA GTTACGACAC TGCAGATTAC ACTGGAATAA  420
CAGGTTTGTG AGGCTATAGT GTGCACCACA TTAACACAGC AAGAAAGAGC TATTTATATA  480
GAAAGGCTGG AATGAGGGAT TTTTACTAAA GCAAATTAAC TTCTTGTCAG CTGCCAAAAC  540
AAAACAAAAC TGAGCATATG AGTGTTAGTA TACTGAAGGC ATGTTATACC AGTTTCTGTG  600
CAGCATGCTA AAAGTTAGAA CTTCTTCACT GGTGCTTATC AATCATTAAT AGTCACGTTT  660
TTGCCCCTTC TTGCCAAATT TCGAGGCATG

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690

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1186 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ACCATAGATT TATTTTAAAA GGGAAAATCT CACACATAAT TAAGCAGTGG AAAATGTGCT 60
CAATGCTATG GTGCGTCAGG CCCTCTGTCT ACCAGGTTTC TCCCGCTTTC TGCAGAGCTG 120
TGGACCCTGT ACGTACCAAA CAGGTGAACT TGGTCCATCT TTCCTTCTTC CTTTTTTTGC 180
ACATTTGCAT TTATATCTTC CTGTACTAAA AGAAACAAAT TATTTATAAT TGGGGTGACA 240
ATATAAAGGA ACAAAGATG GGGCAATAGT TGCTTCCTAG CTGGAGCTGT AAGTCCATGT 300
TACAGAAACT CACTATTTAA AAAGTTTTAA AAGATTTATG AACCTTGTCC TACAATTCGC 360
TGAATACTTA TTTGTCTTTT AAAGTCCCCT CGGTGTATGG ATCATCTTCG TCAGAATGCC 420
GTTGTTTCAT TGTGAATCAG GGGAAAATGT TAATCATTTG GAGACTGTTT TCTTATTACC 480
AAATGTACAA TCCATAAGAC AACTGAAAGC AACAACTGCT GGGTTCCTG ACAAAGATTA 540
TAAAAATCAT CACGTTCAAA GTAGAGTTTT TAGCCAAGGT CAAGAACTAA CCTGGGGCTG 600
AGTCAGCGTC TCTACCCACT TAAATAACAG CGTAAAGATC TTTCACTAAA TTCGTTATGT 660
GGTCTGTCTG GATGTAAACC TATATATTTT CTTTTGAAAC AGAATCATAT CCTGCAGACT 720
CTTGGCACTC CTGCATAGCT TTGACCGAAT GTTCACTCTC ATCGTAATGG AAGATTTCTA 780
TCTATGCAGA TAATACATGT TTTTAAATAC TGTTCCTCTG TTAGTCCTCA ATCTTCCTAA 840
CTCAAATTGG GGACTGAGGA GAGAGAAAGG TGTTACCCC TGTTACCGTG CCATATTCTT 900
CTTGCTGCTT TTCAACCCCA CGTGATTGTT GATTGACGGT TCTGCTATAA TGTGCGTGCC 960
CTTCAAGTTT CAGAAACTT TCCCAATCAT TTCACCTCAA TCTTAATTGA ACCCAAGAGT 1020
CAAAGTTATT ATTTTCTCCG AACGTGTTTG TGATCTTCTG TTATATTTTG GGGCATGTTA 1080
CCTTTATGGT ATATAAGCTG TAGTGCATAC TCTTTGTATT GCAAAAAACT GGTGAGTAAT 1140
TTATGTACAT GTATTCCACA TTTTAGTGTG CTTGAAGTGA CAATCC 1186

```

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

GGGAGAAGGA GGAGGCCGGG GGAAGGAGGA GACAGGAGGA GGAGGGACCA CGGGGTGGAG 60
GGGAGATAGA CCCAGCCCAG AGCTCTGAGT GGTTCCTGT TGCCTGTCTC TAAACCCCTC 120
CACATTCCCG CGGTCCTTCA GACTGCCCGG AGAGCGCGCT CTGCCTGCCG CCTGCCTGCC 180
TGCCACTGAG GGTTCCTCAGC ACCATGAGGG CCTGGATCTT CTTTCTCCTT TGCCTGGCCG 240
GGAGGGCCTT GGCAGCCCCT CAGCAAGAAG CCCTGCCTGA TGAGACAGAG GTGGTGGAAG 300
AAACTGTGGC AGAGGTGACT GAGGTATCTG TGGGAGCTAA TCCTGTCCAG GTGGAAGTAG 360
GAGAATTTGA TGATGGTGCA GAGGAAACCG AAGAGGAGGT GGTGGCGGAA AATCCCTGCC 420
AGAACCACCA CTGCAAACAC GGCAAGGTGT GCGAGCTGGA TGAGAACAAC ACCCCCATGT 480
GCGTGTGCCA GGACCCCACC AGCTGCCCAG CCCCATTGG CGAGTTTGAG AAGGTGTGCA 540
GCAATGACAA CAAGACCTTC GACTCTTCTT GCCACTTCTT TGCCACAAAG TGCACCCTGG 600
AGGGCACCAA GAAGGGCCAC AAGCTCCACC TGGACTACAT CGGGCCTTGC AAATACATCC 660
CCCCTTGCC TGGACTCTGAG CTGACCGAAT TCCCCCTGCG CATGCGGGAC TGGCTCAAGA 720
ACGTCCTGGT CACCCTGTAT GAGAGGGATG AGGACAACAA CCTTCTGACT GAGNAAGCAG 780
AAGCTGCGGG TGAAGAAGAT CCATGAGAAT GAGAAGCGCC TGGAGGCAGG AGACCACCCC 840
GTGGAGCTGC TGGCCCGGGA CTTGAGAAAG AACTATAACA TGTACATCTT CCCTGTACAC 900
TGGCAGTTCG GCCAGCTGGA CCAGCACCCC ATTGACGGGT ACCTCTCCCA CACCGAGCTG 960
GCTCCACTGC GTGCTCCCCT CATCCCCATG GAGCATTGCA CCACCCGGTT TTTCGAGACC 1020
GTGACCTGG 1029

```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 985 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

ATCACTCTTT CTCAGCTCGA CTGGAGTTTC TGCACCTTTG CAGGGGCAAA GTAAGTCCCT    60
GCACCCTGAA CCACCCCCCA TTCCTGTTCA TTTCAGCAGA TAATGATGGA GGGGGGGGGG    120
TGTCCATCGT GCTGAGGGTG TGACCGCAAG AGGGTGAAAA CTTCAGCCA ACTTTCTCAG    180
TCCTTTCTCT TGCAGAGAGG AAGCCACCTG CTATACAAAC TAATACCCCC TGCCTTGACC    240
CCTTCCCCAC GACTCAGTTG ACAGAAGGAT ATACTTTGTT ATAACCTATT ATTTTGTTCT    300
CTGTAAATAC AAGATGTTTA TAGGAAATAT GTATTCTGAA CTCTATCTGC AGAATGAGTC    360
ACTACACCAA AATAGTTCTA TTATTTAGAA TGTGTAAAT TTAAAGGGAC CTGATAGGTA    420
TTTATTTACA TATGCGATCC ACATTGTGT GAAAGCATGT GATCATACTA ACCCAGCCTC    480
CTGGAATGTC GCTGTACGAT GATTGATGTC TTTTCTCAG TCCATAGTTA CAATTGTTTA    540
GTATGCTAAT CAGTCCAGTT CCCTGAGGTT TAAGATCAAA TATAAATTAC TCTGCTTTTC    600
GACTCATTCA GGTAGCATTG TACCTGAACC TGATTGCTAC TTTTTCATCT TAAATATTAT    660
ATTTCCCTCAT CTAATCTGCC TTCCCTCAT CCACAGACAT TTGGAGAAGG AAATGGGAGG    720
GTGTCTGTTA TCCCTTTCTC TTTGCTTTGT CCCCCTGTT AGACTGGCAG CGTCAGTTGC    780
TCGGTGGGCT TGGTTAGAGC CGTGGGTGAG GCAGGTGGCT GCGGGGGACA GGGAGAGGCT    840
GAGAGGGAAG TGGTGGCATT TACTGCTCTG ACACTTCCAC TGTCCCTGCT GGGGATGCTG    900
GGGCCAAGGC CTGTGGGGCC TGTGAAGTGC ACAGCCAGGA GCAAGGAACC CACTAAATAC    960
TCGTCACTG CATGTCCCCT CTACA                                     985

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(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 622 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ATGTTTTTCA TTTTTTTCAT GTTATCTATC CAAGCACTGT TCCATGGTCA GCAAGTCATA   60
TTTCATAATG TGGATTTTCC AAAATAATTA TTGAATACAG CTATTCTATG GCTACTTTTA   120
GTGTTTTTGT GGTATGTGGT GTGGGAGTGT TTATGGAATT ACCAGTATCT TAAATTTTCA   180
AAGGAACCTT GGAAGTCTAT CACTCTAAAT GAAAGTCTGT CACTCTACAT GAATTATGTG   240
CTCAAATTTG ACCAACTCAG TTTAAGACAC AAAACAGTAA TTTGAAGAAG GAAAAATGAA   300
GAGAGTTTCT AGTTTAATGG GTTAAATTTT TGTTGTTGCA ATAGTAAGTT TAGTCTTCTT   360
ATAATATTTT TAAATGAAAA ATCATAGGTA TTTGTTACCA TGTGTGAAGA TTACTTTGTT   420
AAAAGCAAAA GTGGTCGTGT GATATGCTAA ATGTTAATTA CTGATTTTAT ATGTTTAAAT   480
CACGCCAAAC AAATTATGTC TGTGCCATCC AGGGTCTGTT GTTAATCTTT TTCTGAGTAC   540
TTGGATTGGG ATAAAGGGCT TGTACTATGC ACTTTTATT AATGAATAAA TAGAAAACGT   600
TAGTAACAAA AAAAAAAAAA AN                                     622

```

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1129 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

GATTTTTATC TAGAAACTAT ATTTACTTAA ACCCCCCTCA GGAAAGAGGT TTTAAAATCA 60
AAGATGGGAA AATCGGAGAA AATTGCCCTT CCCCATGGCC AGCTTGTTCA TGGTATACAC 120
TTGTATGAGC AACCAAAGAT AAACAGACAG AAAAGCAAAT ATAAGTTGCC ACTAACCAAG 180
ATCACCTCTG CAAAAAGAAA TGAAAACAAC TTTTGGCAGG ATTCTGTTTC ATCTGACAGA 240
ATTCAGAAGC AGGAAAAAAA GCCTTTTAAA AATACCGAGA ACATTAAAAA TTCGCATTTG 300
AAGAAATCAG CATTCTAAC TGAAGTGAGC CAAAAGGAAA ATTATGCTGG GGCAAAGTTT 360
AGTGATCCAC CTTCTCCTAG TGTTCCTCCA AAGCCTCCTA GTCAGTGGAT GGAAGCACT 420
GTTGAAATTT CCAACCAAAA CAGGGAGCTG ATGGCAGTAC ACTTAAAAAC GTCCTCAAA 480
GTTCAAATTT AGATTTTACA TTTCAGTATG TGTGTAAAAC ATAATTTTTC CCATATCCCT 540
GGACTCTTGA GAAATTTGGT ACAGAAATGG AAATTTGCCT TGTTGCAACA TACAATTGCA 600
AAAGATGAGT TTAATAAATT ACATACAAAC AGCTTGATT ATATTTTATA TTTTGTAAAT 660

ACTGTATACC ATGTATTATG TGTATATTGT TCATACTTGA GAGGTATATT ATAGTTTTGT 720
TATGAAAGTA TGTATTTTGC CCTGCCCACA TTGCAGGTGT TTTGTATATA TACAATGGAT 780
AAATTTTAAG TGTGTGCTAA GGCACATGGA AGACCGATTT TATTTGCACA AGGTACTGAG 840
ATTTTTTTCA AGAAACAGCT GTCAAATCTC AAGGTGAAGA TCTAAATGTG AACAGTTTAC 900
TAATGCACTA CTGAAGTTTA AATCTGTGGC ACAATCAATG TAAGCATGGG GTTTGTTTCT 960
CTAAATTGAT TTGTAATCTG AAATTACTGA ACAACTCCTA TTCCCATTTT TGCTAAACTC 1020
AATTTCTGGT TTTGGTATAT ATCCATTCCA GCTTAATGCC TCTAATTTTA ATGCCAACAA 1080
AATTGTTTGT AATCAAATTT TAAAATAATA ATAATTGGGG CCCCCCCTT 1129

```

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 877 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

CACACTGAGG GTTTTAAACA CCATTCTCCC CCACTTCTCT CCTGGGTGAC ATAAGAGAGA   60
AATAACCTGT AGTACAGCAG CTAAAGTATT CTCCTTTCAG AGAATTTTTT TGGAGGTCTC   120
TAATATATAT TTCCCCCTTG TCTCTGTGAT CTCTTATTTA TACTATATTA TTGTCCCATG   180
TACTTTCTAA ACTGAGCTTG GAACATTTAG TATTCCTGCA ATTGGACTTC CCACTTAACA   240
ATTATACAGA CTTTGCTTTT AGAAATAGAT TAGGTTCCAA ACAGAAAGTT CAAGTGTAAC   300
AACAACAATA AAAATAGATT ATGAAACAGG CTATAATTGG CTCTTTTGGA TTTGATAGGG   360
GCAAGATGAA AGGCAACTTT CTTGCTTTTG AAATCATGTT GGGTAAGAGG TAAGGAATCC   420
AGCTACAATT TTATTAGTGC TTGAAACGGG CTTCTTGAA TTCTCCAGGC CCTATCATTT   480
TTTTTTTTCT TACTAATCAG AAGAGAGCTG GGGTAGAAGC CCCATGTTTG TATTCCATGA   540
AACACGTCGG GTTGGAGTAA AGGCAAAAAC AGCTAGACAC ACCAGGTGTG TCTGTTTGAC   600
ATTTATAAGC TGGCACTCAT CAACACTCCT GTTTCTCCTT TCTCTGGGAC GTGTGGATTA   660
AGGGGTGTGA GTTGTGGGAA GAATTGCCCT CGTACCTCCT GGATTTATTA TTTTCTCAA   720
ATACCAACCA GTAAGATCCC AAATAACTTG AGAAAAATTG TTTCTGATC TGTCCACTTC   780
TGGTGTCAA GATTTTACTC ATCTTCTTAG TACATTCTAT GTATTTTATA TGTATAATTT   840
TATACAATTA AAAATAGATT TTTGTCTAGT GAAAAAA

```

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

GTCGGGGAGC GCGGGGCCGG GGCCCAGGGG ACCCCGGGCC ACGGAGAGCG GGAAGAGGAT 60
GGATTGCCCC GCCCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT 120
AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAGAAGT TCAGAAGCAA 180
GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTTGATCTC AGCAGTTTTG ACTTCAGAAC 240
TGGAAAGATG ATGCC TAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT 300
CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC 360
AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA 420
CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT 480
TAGTGATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA 540
AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA 600
CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGGAAAAGA ACCCTGCTGT 660
TTGGCTTAAC ACATCTCAAC CCCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG 720
GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA 780
CATCTTGTCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA 840
AGCCTAAGAA TATGATCAGG TAACTTTCGA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA 900
ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA 960
TAGAGCTTTT TAATAGCACT AACCAATGCC TTTT TAGATG TATTTT TGAT GTATATATCT 1020
ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA 1080
TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG 1140
TAGCACTTAC GTAAAACATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC 1200
TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA 1260
CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCATCA CTGTAAAGAC AAATAAATGA 1320
TTATATTCA

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 697 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

GTAGGCGCTA GTCTGGGCGC AGAGGTTTCT GGGAGCCAAG AGTGGTAATG GCGTCTGTAT 60
GATCTTCGGA GCCTGCTGCA TCGGACCTCG GCCAGTCATA AAAGATGACA ACAGCAGCCA 120
GGCCAACCTT TGAACCTGCC AGAGGTGGAA GGGGAAAAGG AGAAGGTGAT TTGAGCCAAC 180
TTTCAAAGCA GTATTCAAGC AGAGACCTAC CCTCTCATAC AAAGATAAAA TACAGACAGA 240
CTACTCAGGA TGCCCCTGAA GAGGTTCGTA ACCGTGACTT CAGGAGAGAG TTGGAAGAAA 300
GAGAGAGAGC TGCTGCAAGA GAGAAAAATA GGGATCGTCC AACCCGAGAA CATAACAACCT 360
CCTCTTCAGT GTCAAAAAAG CCACGGTTAG ACCAGATTCC TGCCGCCAAC CTTGATGCAG 420
ATGACCTCTT AACAGATGAG GAAGATGAAG ATTTTGAAGA AGAAAGTGAT GATGATGATA 480
CTGCAGCTCT TCTTGCAGAA CTGGAAAAAA TTAATAAAGA AAGAGCTGAA AAGGGCCAAG 540
GCCCAGGGAA GGGACCAAGG GCCAAAAAAG CTTTAAGGGG GGAAGGGTT TCGTTTTGGG 600
AAAACATTGG TTGGGCGGGA AACCTTTCC CTTTAATCTT GAGCTTGGCC CATTCCAAGC 660
TTAAGGCCGA CTTTGAAAAG TTTGAAAGGA GGGTGGG 697

```

(2) INFORMATION ON SEQ ID NO. 61:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

CGAAGAATAG AATTGGCCAG GACCTAGGTT CTCATATTCT TGGTATTCCT CCTGGATGGA 60
AAGGCTGTTG GCATCAATAG GGGACAGAGG CTGATGCTGG AGTGGCCAGT AGAGGTGGTG 120
GAGCAGAGCA GCCATCTTTT AAGTGGGGCT GTATCAGGCT GGGTTTATTT AAAAGCAACA 180
AAATGTTTTG GTTAAGAAAA TTATTTTGCT TTCAGTGTA ATCTTCGCAG TGTTCTAAAC 240
AAAGTTCAGT CTCTGCTCG CCCCTTTCCC TCACTGATGT CTGCACTTGG TTGAGGTCTC 300
CTGGAGCCTC ACAGGCTCTG CTGTTCTCCA CTTCTCACCT GCCATCCACG CCCTGCAAGC 360
TCATGCAAC ACCCTTTCTT CCTCCTGCGG CAGAGTTGTT CAGGTTGCCT GGGCAGGGGC 420
TTAAACAGTG CCAGCCCCTG CCATCCCAAA GCTATTGTTA AGCCCCCAG GCGTCCTCCA 480
CCCACGCCCC CTAGCCTGCC ATGTCCACAG TTCCTTGGGC TGCTGAGGGG CTAGTGCAGT 540
GGTCCTGACC TCTCTTATCA AGAGCACACT TCTTTGCTGG TTGCTCCTTT TGAGCATATG 600
CGTGTGATTA TTTGGAACAG TTAGACTTGC CACGTTGGGT CAGTTTTAGA AATTGTTTCT 660
AGCTAGAGGG ACTGGTGTCC TTCCAAGTCT AGCATTTGGG GTATGGAAAA TTGTTGTGGT 720
GTGTGGTAGG GTTTTTGTTT TCTTTTTTGA GTTTTTTTTC CCCCTTTAGT CTCCTGGCTT 780
TTTCCTTTCC CTTCCTTTCT CCACTGGCCN AGCTTGGGCC TCATCCTCAT GTCATCCTTC 840
TAGGAAGGCG CCTGCCCCAT CTTGTCTGCC GGCAGCATGC ATCCAAGGCC AGAGCTCAGG 900
CCTGCAGACT GGGCTGGTGC CTCCTCCGCT TCAGGGTATG GGAGTTGGTG AAGGGGCTTT 960
CAAAAAATAA TAAGAAAAAA AAGGTAAAGT CTTTGGTAGC TTCTATCCAC TCAGATCCTG1020
GAAGGCAGCA AGGTTTTGTG GATCTAGATT CATTAGGAAT GTCTTCTTGT CAGCCAGGCC1080
AGGACCCGGG CTTGCCAAGA GCAGAGGCCC TCCCAGCAAC CAGGATACCA CCACTTTGGG1140
GGCTTTGTGT ACAGAGGTCC GGGTCTGAGA CCTCATAGGC TGCAGAAATC TGGGGCAGCC1200
ACCATCAAGA AGCCCCTCTC AGGGGCCAGA ACTCCTTTGC CAGCGTGGAT TTCTCAAGTC1260
GGGACTGCAT AATTAAAGCA GTTGCAGTTT TATTTTTTTT ACAGCTTTTT TCCCAAAAAT1320
GATTTGTAGT TGTGTGTGCA GCACTTCGCC CTGATATGTG TGCTCTACAA TAAAAACCA1380
ATCTAATAT 1389

```

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 535 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

TGTATTGAGG TAATAAATTG TTTTACTGAC AATTTTTCCT TTTTCTACAC TAAAACAATA    60
TGTGATATAT TTCCCCTCTT GAAGAGGCAA TTCATTAAAC TCTCAAATTT TCTATAGAAT   120
CAAGATAGAA CCTTTAGATA CTCCAAC TCA CCAAAATGTA AAAAAACTAA CAAAAATATT   180
TGGTCTTCAA TAATGCTAAA TATCTACATT TTTAGAATTT ATCAACATTT AACTAGATAA   240
TTGGGCATGT CTTAATTATG CATGTACTTA TCCATACTAA TAAAATTGAC AATGCTAGTG   300
CATACTTATT GGTTTAGTCC TATTATCAGG ATATAATCAT CTGTGAGGAG GATATTTTAA   360
ATACTGTAAA TGATAACAGT TAATGATATA CACATTTAGA CTGAGTTGCA CACTGGCAGG   420
GAGACCAAAA ACATTACTTC CATACTTG TG TCATGATTCT TTTTTTTT TG AGAGAGTCTC   480
ACTCTGTCGC CAGGCTGGGA GTACAGTGGC ATGATCTCGG CTCACTGCAA CCTCT      535

```

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

GTGATTTGAC  ATTTGAACAA  ATTAGGAAGC  TGAATCCTGC  AGCAAACCAC  AGACTCAGGA  60
ATGATTTCCC  TGATGAAAAG  ATCCCTACCC  TAAGGGAAGC  TGTTCAGAG  TGCCTAAACC  120
ATAACCTCAC  AATCTTCTTT  GATGTCAAAG  GCCATGCACA  CAAGGCTACT  GAGGCTCTAA  180
AGAAAATGTA  TATGGAATTT  CCTCAACTGT  ATAATAATAG  TGTGGTCTGT  TCTTTCTTGC  240
CAGAAGTTAT  CTACAAGATG  AGACAAACAG  ATCGGGATGT  AATAACAGCA  TTAACACACA  300
GACCTTGAG  CCTAAGCCAT  ACAGGAGATG  GGAAACCACG  CTATGATACT  TTCTGGAAAC  360
ATTTTATATT  TGTATGATG  GACATTTTGC  TCGATTGGAG  CATGCATAAT  ATCTTGTTGT  420
ACCTGTGTGG  AATTTTCAGCT  TTCCTCATGC  AAAAGGATTT  TGTATCCCCG  GCCTACTTGA  480
AGAAGTGGTC  AGCTAAAGGA  ATCCAGGTTG  TTGGTTGGAC  TGTTAATACC  TTTGATGAAA  540
AGAGTTACTA  CGAATCCCAT  CTTGGTTCCA  GCTATATCAC  TGACAGCATG  GTAGAAGACT  600
GCGAACCTCA  CTTCTAGACT  TTCACGGTGG  GACGAAACGG  GTTCAGAAAC  TGCCAGGGGC  660
CTCATACAGG  GATATCAAAA  TACCCTTTGT  GCTAGCCCAG  GCCCTGGGGA  ATCAGGTGAC  720
TCACACAAAT  GCAATAGTTG  GTCACATGCAT  TTTTACCTGA  ACCAAAGCTA  AACCCGGTGT  780
TGCCACCATG  CACCATGGCA  TGCCAGAGTT  CAACACTGTT  GCTCTTGAAA  ATCTGGGTCT  840
GAAAAAACGC  ACAAGAGCCC  CTGCCCTGCC  CTAGCTGAGG  CACACAGGGA  GACCCAGTGA  900
GGATAAGCAC  AGATTGAATT  GTACAATTTG  CAGATGCAGA  TGTAATGCA  TGGGACATGC  960

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ATGATAACTC  AGAGTTGACA  TTTTAAACT  TGCCACACTT  ATTTCAAATA  TTTGTACTCA1020
GCTATGTTAA  CATGTACTGT  AGACATCAAA  CTTGTGGCCA  TACTAATAAA  ATTAATAAAA1080
GGAGCACTAA  AGGAAAAA

```

1098

(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TAAGATCCTG	ACTCTGAAGC	TTCAAAGTGA	CACTGTGGAA	ATCTGAAACG	AGGGGATGTC	60
ATGAAGGCAG	CTTTTCTTTT	TCTGAGGAAA	AAATAGGCAT	GGGCTACAGG	ACTATTTAAA	120
ATGTCTCATT	TACAGTATAA	AACTCAAAGG	TAGATGTAAT	TTTACACCT	ATGAGTATTT	180
GTCCAATTTT	TGTCTCTTCC	TCACCATTGG	GTATCTATT	TTTATATGTA	AATAAGATAA	240
GGTCATCTGA	TAGCCTTATT	CAGTCTTCAT	CATTTTCATC	ATTGTTCCCTA	TGTAGATTAT	300
TGGACATTTA	TTGTAGCACT	ACATAACTGA	TTATAAAAAT	CTGTAAATGA	ATTAGCACTT	360
TCATATTGAA	ACAAGCCTGC	TAGCCTATGT	ATAAAATAGC	AAAATGTTTG	CTGTTTATAA	420
AAAGATGTAA	TGGGGTGGGG	GGCAGGGGTA	ATTTCAAGTT	ATTAATTTAA	AAATGAACATA	480
GCAATTTTGT	ACCTGGTGAC	TTTGTGGTGC	ACTCACCTCT	GATAGTGA	TGAATTCGGT	540
ATGTAAAAAG	GGGTAGTGG	TATTTTCATTG	CTGCTAAAAA	TGACAACTCC	CTCTGTGTCC	600
TGTTTTTCTT	AAAGCTGTCA	GTGTACAAGT	GGGTATTTGA	ATACCAGACC	TTACTGTAAA	660
AAATAAAAAA	GGTGGTATCT	AGAGCATGTA	AATTGGATAT	AAAGTTCCTGC	TCTTAAAGAG	720
TTGATCTAAG	AGTATGGCTA	AACATCTATA	TATGCAATCT	ATTAAAAGAA	CCTTAATTCGG	780
CTATTATGTC	TTGATTTGAT	TGCAGTTTTT	TCCTAATTAT	AACAAATTTT	TCCTCATTGG	840
CCTGTTTTTA	ATCCTGTGCC	TAGAAGGAGT	ACAAAATGCA	CACTTTACAA	AATTGATATT	900
TAACACTTAC	CCACTCCCCT	TTCCCCATCT	CTTCTACCGC	TCTTGTTGAT	CGTGGTATCT	960
GATCTTGACT	AGATAGGCTG	AAGGCACATG	GTTCCCTCCA	AAAACCACTA	TTGATACCAC	1020
TACAAAAACA	AGCCAGCAAA	AAGATACTGT	AGAGAGGTTG	GCTTGCTTCC	CTCTCTTCCT	1080
AACTGCATGT	TGAAAAATAA	GCCGTTATTG	ATCTTAAACA	TCGGTCAGAT	GAGTCATACA	1140
TTGGGTTATT	TTTTATATAC	ATGTATACAC	AAAATATTTT	AAATTGAAAG	CAACATCTTA	1200
ATGGATTCAA	AACTATTACA	AGCTGTTGTC	TAAAACAGGT	GAGAAAAAAA	TTTATAACTG	1260
TAAAAACAAA	TGCACATATT	GATATTTAAA	ATGCGTAATT	AAGAAAACCC	ATTGTTGTTG	1320
TGTTTTTCTT	GTATACCAAT	AATTAAGCCA	CTACTGTTGG	CACTGTTTGG	TTTTCTATTT	1380
TAACACTGAA	GGAGTGAAAG	TATTTCCCTAT	ATTTATGAAT	TTACTACTAA	AATCTTGGCA	1440
AAAAAAGAAA	AAAATTGTCT	AACGTGTGTG	GGTGAAACT	GTTAATCAAG	TGTTTCTACT	1500
CCCCCCCCGAA	AATCCCCTGA	AAGTTGGACA	CCAAGTGTAT	ACCCTAGGTT	GCTTAAAGGG	1560
ATTTCACTAT	TATATAAAGT	CAATAAAAAT	GAAGTAGTTG	TATATATGCA	ACATTGTGTA	1620
CAGAGGGGAA	ATAATGAATA	GTATTAAAGA	AACATTCTCG	TCTTCCTTTA	CCTTTAATCC	1680
CCTAATACCT	AGTCTACTTT	TTAAATTTTC	AGACTTCACT	GCTTTTTTGA	TTCATAATTC	1740
TAATTTTTCAC	ATTATTGTTA	ATGGAAAATC	ATATCTAATA	AAGGTTTTAG	TTATTCCCAT	1800
GCACAGTATG	AAAATTCTCA	TTTGCTGAGG	TTTTGTTTCA	AGAAAATGTA	TTGGCATGTC	1860

(2) INFORMATION ON SEQ ID NO. 66:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CRTWSILRGR MWLSTNSAAD AINPWGRSS RPRSRAAVPH RLLHLPPVCA ELQGQQFYSL 60
 EGAPYCEGCV TDTLEKCNCT GEPITDRMLR ATGKAYHPHC FTCVVCARPL EGTSFIVDQA 120
 NRPHCVPDYH KQYAPRCSVC SEPIMPEPGR DETVRVVALD KNFHMKCYKC EDCGKPLSIE 180
 ADDNGCFPLD GHVLCRKCHT ARAQT 205

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AARALKRPFP SGPPLRDRSP SLESQSRKTP RLPEDLASGK KDYTFQRPLR RRDRKRRASR 60

VSLRVDPSDH GGPGVVADEV PHQGKCGWGR RLPGVVRPGAA GAQRQEPGSP TEGWGGGPPR120
 HVPVQPVRVS ADRPADTPAP SPSKDLLSHP 150

(2) INFORMATION ON SEQ ID NO. 68:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

LLECRHHDGD VSSVGGPLQG PRVLQGG LGV CEGAHQVASQ QGRLPRPERA GLPLT 55

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 182 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

SVHFPAALRC ETAALLWSLR AARHHDSQRT LRRARKTTPS RGLCGAATGS GGRAECPCAW 60
IRATMVARVW SLMRFLIKGS VAGGAVYLVY DQELLGPS DK SQAALQKAGE VVPPAMYQFS120
QYVCQQTGLQ IPQLPAPPKI YFPIRDSWNA GIMTVMSALS VAPSKAREYS KEGWEYVKAR180
TK 182

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 25 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

PEDSGLGPHS EGRPPDCRPN KGLQK

25

(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 56 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

DEKNTSFLYS DVGATSMKSV LYESYTKMGR HLVNCARYLK CMFRKAFYQL RNMTYF 56

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 291 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

LERLVDIKKG NTL LLQHLKR IISDLCKLYN LPQHDPVEML DQPLPAEQCT QEDVSSEDED 60
EEMPEDTEDL DHYEMKEEEP AEGKKSEDDG IGKENLAILE KIKKNQRQDY LNGAVSGSVQ120
ATDRMLKELR DIYRSQSFKG GNYAVELVND SLYDWNVKLL KVDQDSALHN DLQILKEKEG180
ADFILLNFSF KDNFPFDPPF VRVSPVLSG GYVLGGGAIC MELLTKQWS SAYSIESVIM240
QISATLVKKG ARVQFGANKS QYSLTRAQQS YKSLVQIHEK NGWYTPPKED G 291

```

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

RSVVRRLKLM AAEEPQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60
LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSL EALLDDSKEL120
QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALS VSI240
QVEYMDRGEG GTT 253

```

(2) INFORMATION ON SEQ ID NO. 75:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 108 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

EKFLNMGAPL GVGLGLVFVS SIGIYVSSTY PPVAGATLYS VAMYGGLVLF SMFLLYDTQK 60
VIKRAEVSPM YGVQKYDPIN SMLSIYMDTL NIFMRVATML ATGGNRKK 108

```

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

MHRDSCPLDC KVVYVGNLGNN GNKTELERAF GYGPLRSVW VARNPPGFAF VEFEDPRDAA 60
DAVRELDGRT LCGCRVRVEL SNGEKRSRNR GPPPSWGRRP RDDYRRRSPP PRRRSPPRRS 120
FSRSRSRSLs RDRRRERSLS RERNHKPSRS FRSRSRSRS NERK 164

```

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

EAALTCHLL SSWVSLESIT LSYNGLGSNI FRLLDSLRL SGQAGCRLRA LHLSDLFSPL 60
PILELTRAIV RALPLLRLVLS IRVDHPSQRD NPGVPGNAGP PSHIIGDEEI PENCLEQLEM120
XISTGSPASP TAVLRSEGLG FSAAAVPG 148

```

(2) INFORMATION ON SEQ ID NO. 90:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```
EDGADGAFYP DEIQRPPVRV PSWGLEDNVV CSQPARNFESR PDGLEDSEDS KEDENVPTAP 60
DPPSQHLRGH GTGFCFDSSF DVHKKCPLCE LMFPNYDQS KFEEHVESHV KVCPMCSEQF 120
PPDYDQQVFE RHVQTHFDQN VLNFD 145
```

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 282 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
DKSSACRRNG NYSDEKKDAM YWEKRRKNNE AAKRSREKRR LNDLVLENKL IALGEENATL 60
KAELLSLKLK FGLISSTAYA QEIQKLSNST AVYFQDYQTS KSNVSSFVDE HEPSMVSSSC120
ISVIKHSPQS SLSDVSEVSS VEHTQESSVQ GSCRSPENKF QIIKQPEMEL ESYTREPRDD180
RGSYTASIYQ NYMGNSFSGY SHSPPLLQVN RSSNSPRTS ETDDGVVGKS SDGEDEQQVP240
```

```
KGPIHSPVEL KHVHATVVKV PEVNSSALPH KLRIKAKAMQ IK
```

282

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```
MASLGHILVF CVGLLTMAKA ESPKEHDPFT YDYQSLQIGG LVIAGILFIL GILIVLSRRC 60
RCKFNQQQRT GEPDEEEGTF RSSIRRLSTR RR 92
```

(2) INFORMATION ON SEQ ID NO. 93:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
WTGTGRGAVA IMADPDPRYP RSSIEDDFNY GSSVASATVH IRMAFLRKVY SILSLQVLLT 60
TVTSTVFLYF ESVRTFVHES PALILLFALG SLGLIFALT LNRHKYPLNLY LLFGFTLLEA 120
LTVAVVVTSM MYILSASFHT 140
```

(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```
FFPLLLPLHT PVAGRNLGFP ESLGVPPFLP HPGGTPRAPG LFLLLFSFWA V
```

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

FFLYSFPFTP PWLEGTASL KAWGSHPSYP TREERPGPRA CFSSCFPGQ FDH

53

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

PLDCATFVFV FLNFFKPRMI SPASFSSPSS QTEFKGHFSS SFWHLQPQSG IF

52

(2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

PFSSSVSFFG TAPSCLEGGW ILVCALDRYR INTCALRTGS PRFIQSAHYR KLLCQNPBGD 60
PTPGSPSSLL TSTRAVLLFF ILLFYCFCCG HYHWQSSFSP FLDIGVLSLK DSTLRLKVPK120
AA 122

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 126 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

LFFFCFLFWD CAIMFIRRLD FGVCSRQIQN KYLRLENRKS TIHTKCSLQE VAVSKSRQGP 60
NSGQPLLPAD LNKGCATVFEY FIILLLLLWS LSLAKFLFPE PGHRGPVFEK FHSEAEGAKS120
CLRSGL 126

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 73 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

IDFEGKERGK GQGRDTPPLP LSWAQLGGG RERIFTFEKL LFSEWNKLGQ GAQALSSVPH 60
TPLLRSFIQK NIS 73

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

IRGRREGRV RVETPLPCPF PGPRSWGEGG KGFLHFLNCY FLNGTSWAKG PRPCPLSLTP 60
LCSVHSFKKT FLEHLLCPAY ARPTS*VCVG GLYASSSVPP CPSFTGAFGG SVGGGTFCGV 120
WGSPGSPTKL SPSPVPTHLL QPPA                                     144

```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

CRPTIFTPRP PALGEGSTTT SPLDIPLGTG MWVPLTVRPW GEPKALTSGI AMLGGGASET 60
VGRQDILGAA PSQQGIRQGA VGDGLAQQKG TAWSGFLEIP KPHRRSHLLQ IPQRHR    116

```

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

22

RMGKEALMSW RRDPPTLSW WA

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GAGPWEAFPD GIGRRSRRAR LPQYKRPPGG GGGGDSGRN MAVADLALIP DVDIDSDGVF 60
 KYVLIRVHSA PRSGAPAAES KEIVRGYKWA EYHADIYDKV SGDMQKQGCD CECLGGGRIS 120
 HQSQDKKIHV YGYSMAYGPA QHAISTEKIK AKYPDYEVTW ANDGYL 65

(2) INFORMATION ON SEQ ID NO. 111:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

PSSPSLPVLR AGLRPFCDVL PGCVCVRFLC SCL

33

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 31 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ETCAGAGRCA ADGGNGSGSR VPPASRCCAL G

31

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 67 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

KRAQAPAAAL QMAEMDPVAE FPQPPGAARW AEALLRCFTW LRLCQISMFL SLKCLNTRSS 60
HLGAHCR 67

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GCVAGSAGLS RKSPWTEVET ETFLGSPRYS RRVRSYWLL GLMAVRASFE NNCEIGCFAK 60
 LTNTYCLVAI GGSENFYSVF EGELSDTIPV VHASIAGCRI IGRMCVGNRH GLLVPNNTTD 120
 QELQHIRNSL PDTVQIRRV ERLSALGNVT TCNDYVALVH PDLDRETEEI LADVLKVEVF 180
 RQTVADQVLV GSYCVFSNQG GLVHPKTSIE DQDECLSFQV PCCGDVNEAL SDSWDVYNVS 240
 FVPETT 246

(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

MGYNLSPQFT QLLVSRYCPR SANPAMQLDR FIQVCTQLQV LTEAFREKDT AVQGNIRLSF 60
 EDFVTMTASR ML 72

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

EHTHRCSDQL RLATVSNSVA SKREVYLCPA IGH LG

35

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATLWLAKEKF ICAQPLVTLG DAPDSRQMLV HWPSSSFLK

40

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

QKRSLEFVPSH WSPWVMHQIA GRCWFIGLRP LSS

33

(2) INFORMATION ON SEQ ID NO. 120:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

LSSRSFIST SWGAFVFFCL LSCGSLVLAG FEGASTMAV FSFWASRICW RSFLRFFPDS 60
 VMLARALDAR FLRWCRVISP WSITAPTTRC LRRRSRENTR RRLNSFFFSS VRGRLIFPPG 120
 APIVAIPLQF TVRTSAQRRI RGLRPGLPRA NRNSGAGPRA I 161

(2) INFORMATION ON SEQ ID NO. 121:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

FFQSARALLQ MELTAREALL QSFFCTFFPP KDIPLGEVSR PLGRRKSGE

49

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

KGALLLSKSS ETTTESEGWL QLRIF

25

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

WKRFSSHLQG PSFLHPGGLL SSFAF

25

(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

WLLQLKPHLL AHHPKGLPH RGAPLYSPRT RPRVAIGPRK AGAEPADPAL SGSTDRELEW 60
 NRDYGSSGGK DQPAPNGAEE EAVQTPAGVE SGAASEAPGG RGCDRPRADH AAPPQEAGVQ 120
 CTCQHYTVRE EAQKTTPADP ACPEREDSHG SGSPFKASQD 160

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

FFFPCQPFIF SGTHEVQLVP GTVHSLKQLK GLSPDTPATL SRMHGPGTLT SMEEVGSARG 60
 GRMVARDTES LVLGLWLS 78

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CALLPPTPSR TEP SLHSTGD SGKGAEDRQE AHRDRPTGSQ AAPEERDIQ TEESLPAPHSF 60
QDEKNLPPPP DTDAREVGGR SGKFPFPVPP RTSEPSMLNF FFIKITFIL 110

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

SLPADVPCCP PPHPAQNHPC IPQGTRARVP KIDKRHTETD QLAARQPQRR ETFRQRKVSL 60
PLIPSKMRKT CRHPPTLMPG RWEEEVGNFP SQYPQERLSL QC 102

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 31 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

LCQLMCPVAP HPIPHRTIPA FHRGLGQGCR R

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

GFRPARCDPV PLPTTRSVAG LPVGRVRQLS RPLLGPD TGS VANIFKGLVI LPMSLVIRN 60
QORVIPIRRA PLRSKIEIVR RILGVQKFDL GIICVDNKNI QHINRIYRDR NVPTDVLSEF 120
RHEHLKAGEF PQPDFPDDYN LGDIFLGVEY IFHQCREDED YNDVLT 166

```

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

FDPKLLEGKV KEDPDQGESH KPLTFARFYL PILVPSAKKA IYMDDDVIVQ GDILALYN TA 60
LKPGHAAAFS EDCDSASTKV VIRGAGNQYN YIGYLDYKKE RIRKLSMKAS TCSFNPGVFV 120
ANLTEWKRON ITNQLEKWMK LNVEEGLYSR TLAGSITTPP LLIVFYQQHS TIDPMWNV RH 180
LGSSAGKRY S PQFVKA AKLL HWNGHLKPWG RTASYTDVWE KWIYIPDPTGK FNLIRRYTEI 240
SNIK

```

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

PSFIIHSNPI WLGALLWVSH CPSSILGSLR PRGGKIQLRV GGSEPCRIMK ATCFGNDLPL 60
 PVV 63

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

DYLRSSGFC QNTPLTESTE GMGVGGLGRV RLECEGSLIY AELKSPSLYV HTFVLFSRLI 60
 LAIPNPLPR 69

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

QPFYFNTPL SILHFPHLSK LNLVHRVGLC MCMQEVGVDS ALGWNPP

47

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

VPPCPQLREL CPGVNNQPYL CESGHCCGET GCCTYYYELW WFWLLWTVLI LFSCCCAFRH 60
 RRAKLRLQQQ QRHVEINLLA YHG 83

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

WKSQQLHRML LTRTEFWYLS TEVSTMFTCK RLRKKPLKWT GIQSSFSVTH QSDKRLVTTL 60
 PGLFSFYNSS SIHNDFVLCS IFFNPLSI 88

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 21 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CYMHFLTFVK NVTIVKKCTK M

21

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 58 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

MEIEQVHFPA YRQLYTDLNI FSSCLVKVKE KGFFLPQDIT FFYITSITHH CFWWKSAE 58

(2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

NSFLTQMMVL QNNKMAEHFH K

21

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

SVTKSGFLIP CHLGDFILLC CFKIQCREVV DCRGNKVNSN FEKK

44

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

NPPNDKVSEI QTSLSHSICEN VQPFYCSVKE PSSGSKMNSI NQRIFYTLEK KISSNILTEY 60
CKLHFSS 67

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

KVHTILHFST KSSGVLCLLY KKKLYPVAGK TLSLSLLINN WRKCSSLYKV AYKLESELVQ 60
SPFTF 65

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

KIWSREQNHC EWMNCKMKK VQAKLLQVFC HFDESQKMNF GYLSTLRVFS LIFCM

55

(2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

IPEDPHIDES KAKHQAIIMS TSLRVSPSIH GYHFDTASRK KAVGNIFENT DQESLERLFR 60
 NSGDKKAEER AKIIFAIDQD VEEKTRALMA LKKRTKDKLF QFLKLRKYSI KVV 113

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

MQHFAATLQA SLLSGLQRLR RDRDWKGTRT EQTGYKDSKQ FHALCCYRGE QNAFSKDLKT 60
 LPSLQERIDA DRRAWTDVMR TKENDGWR 88

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

VVEGPDGHH GDAGAEVPRC LWPRSGICGR ECGLGDRWFL RVEDRQDLNR QRIQRYAQAF 60
 HIRGSEDLK DSVEKLELGC PFSPHLSLPM PSVSRSTSR SANWERLRQG TLRRDLRGII 120
 NIGLEDGESW EYQI 134

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

MKVSALLCL LLIAATFIPQ GLAQPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP 60
 KEAVIFKTIV AKEICADPKQ KVVQDSMDHL DKQTQTPKT 99

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

VFFFTAENWW YFHIHSVSIQ FQYPHLMRKK CFTNEGGILK LAVMLGWRKF GI

52

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

FFFLQKIGG IFTFIVFLSN FSTHI

25

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ISCNVRLEKI WYLG YFQGTI KSDFCFFVKK NFFNQYCFYK

40

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

ANYCIHHKL KKRTCIRRLK TRKKIQHPNM YSQEGNQFCN RTGIMNYKQE GVEKEEEKMC 60
EFKTL 66

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 23 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PCCEVLAVGV NWWKCSQQVC WGV

23

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

PAVKSQVLV MCGNAVSKFA GEFDKSIKQN KKSLGIILFH DFFCSFTPEG RNLQQVVEE 60
 EGGEQVY 67

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

EGEPACSGIQ ARRVTPCPSP RDASPAPASE TSLSVPATLV GGSDLIHFQV GSGPTPGPAE 60
 DRAARPSWLT LQLALGWGGR ELMSVASLSW GFPACPVVSC PRCYRGCA 108

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

FCSTTSSVAL HQKEGMGYSR

20

(2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

IPGLKYFVGI AYYIILADEP QDNGYRHTHT YHTKSQLLK SGLGIRLLCP VKNSCTEVIV 60
 1 61

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LMNLRTTATD THIHTRTQNL SC

22

(2) INFORMATION ON SEQ ID NO. 164:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 37 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSGQRLQTHT YIHAHKISAV EEAWNQTSV SSKKLLH

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 72 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TVPFVSASG FHLIFFALPI LFQPVAKNHE TRQWKHRHRR RGPSCALKAG KTASGAGEVV 60
RCLSEQSVAI SR 72

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

LISTSEEVLT FSMLHRNWYN MPSVY

25

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

LKLLAWSYLH SFCVLFASCI

20

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

LLACCTETGI TCLQYTNTHM LSFVLEWQLT RS

32

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

IALSCCFNVV HTIASQTCYS SVICSVVTKV TGLVLFAQFL RLVCFLHLIN

50

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

EHYTIGFQYC THKIHTCVQK VSSSRLVIPF TWKINEGNLY ILYKNKSKFI Y

51

(2) INFORMATION ON SEQ ID NO. 173:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 239 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

EFIHFRNNTN NWREIPENLM DQYSEVNAIS TACSNGVPEC EEMVSGLFKQ WMENPNNNPI 60
 HPNLRSTVYC NAI AQGEEEE WDFAWQFRN ATLVNEADKL RAALACSKEL WILNRYLSYT 120
 LNPDLIRKQD ATSTIISITN NVIGQGLVWD FVQSNWKKLF NDYGGGSFSF SNLIQAVTRR 180
 FSTEYELQQL EQPKKDNEET GFGSGTRALE QALEKTKANI KWVKENKEVV LQWFTENSK 239

(2) INFORMATION ON SEQ ID NO. 183:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 109 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

YANQSSSLRF KIKYKLLCFS THSGSIVPEP DCYFFILNII FPHLICLPLI HRHLEKEMGG 60
 CLLSLSLCFV PVVRLAASVA RWALEPWVR QVAGGDRERL RGKWWHLLL 109

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

SLFLSSTGVS APLQGQSKSL HPEPPPIPVH FSR

33

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

HSFSARLEFL HLCRGKVSPC TLNHPPFLFI SADNDGGGGV SIVLRV

46

(2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

VEGTCSDGVF SGFLAPGCAV HRPHRPWPQH PQQGQWKCQS SKCHHFPLSL SLSPPATCLT 60
HGSNQAHRAT DAASLTGTGK QRETDNRHPP ISFSKCLWMR GRQIR 105

```

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

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RGHAVTEYLV GSLLAVQFT GPTGLGPSIP SRDSGSVRV NATTSLSASP CPRQPPASPT 60
ALTKPTEQLT LPV 73

```

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

MFIFFMFLSI QALFHGQQVI FHNVDFFPK

28

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 65 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ELNTAILWLL LVFLWYVVWE CLWNYQYLKF SKEPWKSITL NESLSLYMNY VLKFDQLSLR 60
 KKTVI 65

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 30 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CFSFFSCYLS KHCSMVSKSY FIMWIFQNNY

30

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

FFVVTNVFY LFINKKCIVQ ALYPNPSTQK KINNRPWMAQ T

41

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

YKFFIPIQVL RKRLTTDPGW HRHNLFGVI

29

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SSHMVTNTYD FSNRNIIRRL NLLQQQKFN PLN

33

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TPLRKEVLKS KMGKSEKIAL PHGQLVHGIH LYEQPKINRQ KSKYNLPLTK ITSAKRNNEN 60
 FWQDSVSSDR IQKQEKKPKF NTENIKNSHL KKSAPFLTEVS QKENYAGAKF SDPPSPSVLP 120
 KPPSHWMGST VENSQNQREL MAVHLKTLK VQT 153

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 304 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

SLYYYGIRDL  ATVFFYMLVA  IIIHAVIQEY  MLDKINRRMH  FSKTKHSKFN  ESGQLSAFYL  60
FACVWGTFIL  ISENYISDPT  ILWRAYPHNL  MTFQMKFFYI  SQLAYWLHAF  PELYFQKTKK  120
EDIPRQLVYI  GLYLFHIAGA  YLLNLNHLGL  VLLVLHYFVE  FLFHISRLFY  FSNEKYQKGF  180
SLWAVLFVLG  RLLTLILSVL  TVGFGLARAE  NQKLDFTGN  FNVLAVRIAV  LASICVTQAF  240
MMWKFINFQL  RRWREHSAFQ  APAVKKKPTV  TKGRSSKKG  ENGVNGTLTS  NVADSPRNKK  300
EKSS                                              304

```

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 198 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

KMTTAARPTF  EPARGGRGKG  EGDLSQLSKQ  YSSRDLPSHT  KIKYRQTTQD  APEEVRNRDF  60
RRELEERERA  AAREKNRDRP  TREHTTSSSV  SKKPRLDQIP  AANLDADDPL  TDEEDEDTEE  120
ESDDDDTAAL  LAELEKIKKE  RAEKGQGPCK  GPRAKKALRG  GRVSWFENIG  WAGNPFPLIL  180
SLAHSKLKAD  FEKFERRV

```

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 55 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

VLIFLVFLLD GKAVGINRGQ RLMLEWPVEV VEQSSHLLSG AVSGWVYLKA TKCFG

55

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SPGFFLSLPF STGXAWASSS CHPSRKAPAP SCLPAACIQG QSSGLQTGLV PPPLQGMGVG 60
GAFKK 66

(2) INFORMATION ON SEQ ID NO. 204:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 161 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

HLGYGKLLWC VVGFLFSFLS FFSFSLAF SFPFSPPLAK LGPHPHVILL GRRLPHLVCR 60
QHASKARAQA CRLGWCLLRF RVWELVKGLS KNNKKKKVKS LVASIHSDPG RQQGFVDLDS 120
LGMSSCQPGQ DPGLPRAEAL PATRIPPLWG LCVQRSGSET S 161

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

LDLVFIVEH TYQGEVLHTQ LQIIFGKKAV KIKLQLL

37

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

ENYFAFSVNL RSVLNKVQSS ARPFPMSLMSA LG

32

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

CMLQINLYFF PLGFSKNTT STPNEHGTCL FLPLLIYSRF SSVFFSNAAF SCSSGLLSGS 60
IVAKDSIRST LHSDVKHSHC LDSSSFLSSN SITDKASVLT DE 102

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 34 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

VLFSKEYVID LQVSSRISAK ASGSACSSSK SINP

34

(2) INFORMATION ON SEQ ID NO. 209:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 43 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

VAHWQGDQKH YFHTCVMILF FLRESHSVAR LGVQWHDLGS LQP

43

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

DLTFEQIRKL NPAANHRLRN DFPDEKIPTL REAVAECLNH NLTIFFDVKG HAHKATEALK 60
KMYMEFPQLY NNSVVCSEFLP EVIYKMRQTD RDVITALTHR PWSLSHTGDG KPRYDTFWKH 120
FIFVMMDILL DWSMHNILWY LCGISAFMLQ KDFVSPAYLK KWSAKGIQVV GWTVNTFDEK 180
SYYESHLGSS YITDSMVEDC EPHF                                     204

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(2) INFORMATION ON SEQ ID NO. 214:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

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SFKVTLWKSE TRGCHEGSFS FSEEKIGMGY RTI

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33

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

NSKVDVIFTP MSICPISVSS SPLGIYSLYV NKIRSSDSLI QSSSFSSLFL CRLLDIYCST 60
T 61

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 24 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PMYKIAKCLL FIKRCNGVGG RGNF

24

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1880 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGCCGGGGGC	CGGGGGCGGC	CCAGGGGGGG	GCCCGGGGCC	GGGGCCCTGC	CTGAGGCGAG	60
AGCTGAAGCT	GCTCGAGTCC	ATCTTGCCAC	CGCGGCCACG	AGCGCTTCCG	CATTGCCAGC	120
GCCTGCCTGG	ACGAGCTGAG	CTGCGAGTTC	CTGCTGGCTG	GGGCCGGAGG	GGCCGGGGCG	180
GGGGCCGCGC	CCGGACCGCA	TCTCCCCCCA	CGGGGGTTCG	TGCCTGGGGA	TCCTGTCCGC	240
ATCCACTGCA	ACATCACGGA	GTCATACCCT	GCTGTGCCCC	CCATCTGGTC	GGTGGAGTCT	300
GATGACCCTA	ACTTGGCTGC	TGTCTTGGAG	AGGCTGGTGG	ACATAAAGAA	AGGGAATACT	360
CTGCTATTGC	AGCATCTGAA	GAGGATCATC	TCCGACCTGT	GTAAACTCTA	TAACCTCCCT	420
CAGCATCCAG	ATGTGGAGAT	GCTGGATCAA	CCCTTGCCAG	CAGAGCAGTG	CACACAGGAA	480
GACGTGTCTT	CAGAAGATGA	AGATGAGGAG	ATGCCTGAGG	ACACAGAAGA	CTTAGATCAC	540
TATGAAATGA	AAGAGGAAGA	GCCAGCTGAG	GGCAAGAAAT	CTGAAGATGA	TGGCATTGGA	600
AAAGAAAAC	TGGCCATCCT	AGAGAAAATT	AAAAAGAACC	AGAGGCAAGA	TTACTTAAAT	660
GGTGCAGTGT	CTGGCTCGGT	GCAGGCCACT	GACCGGCTGA	TGAAGGAGCT	CAGGGATATA	720
TACCGATCAC	AGAGTTTCAA	AGGCGGAAAC	TATGCAGTCG	AACTCGTGAA	TGACAGTCTG	780
TATGATTGGA	ATGTCAAAC	CCTCAAAGTT	GACCAGGACA	GCGCTTTGCA	CAACGATCTC	840
CAGATCCTCA	AAGAGAAAGA	AGGAGCCGAC	TTCATTCTAC	TTAACTTTTC	CTTTAAAGAT	900
AACTTTCCCT	TTGACCCACC	ATTTGTCAGG	GTTGTGTCTC	CAGTCCTCTC	TGGAGGGTAT	960
GTTCTGGGCG	GAGGGGCCAT	CTGCATGGAA	CTTCTCACCA	AACAGGGCTG	GAGCAGTGCC	1020
TACTCCATAG	AGTCAGTGAT	CATGCAGATC	AGTGCCACAC	TGGTGAAGGG	GAAAGCACGA	1080
GTGCAGTTTG	GAGCCAACAA	ATCTCAATAC	AGTCTGACAA	GAGCACAGCA	GTCCTACAAG	1140
TCCTTGGTGC	AGATCCACGA	AAAAACGGC	TGGTACACAC	CCCCAAAAGA	AGACGGCTAA	1200
CCCTGGAGTA	TCACCCCTTC	TCCCTCCCCA	GGCACCACCTG	GACCAATTAC	CTTTGAATGC	1260
TGTATTTGGA	TCTCACGCTG	CCTCTGTGGT	TCCCTCCCTC	ATTTTTCCTG	GACGTGATAG	1320
CTCTGCCTAT	TGCAGGACAA	TGATGGCTAT	TCTAAACGCT	AAGGAAAAAA	AACAAACACA	1380
GAAGTGTTC	AAGTACTCAA	GACTGACTTA	CAGACCAACC	AACCACCTTG	CTGGAACCCT	1440
TGCTAGCAGG	CATTCTTATA	AAAGAAACTT	TCGAGCCTCC	TTATATTGCT	GGAAACTCAG	1500
CTGTGCTCCA	GACTAGAGCC	TCCTTACCTA	TGCTATGGAT	TTTTAATTTA	TTTTCTCTTA	1560
TTTCATGTAC	ACTGCTTTTT	TTGGTTACAG	TGTATGATGG	ATGTGTATGA	AAAAATGTA	1620
TCTTTGGGAA	AACAATTACA	GTTTGTTAAT	TTGGAAAAAA	AAAAATGAC	TCATCTTTAT	1680
TTTTATTTCG	ACATCCCACC	CCATCCCCTG	GAAGTACTTG	GGGAGGTGGG	GAGGGGTACG	1740
AGTCCACTGT	TGGCTTGGTA	GGAGATGAGA	GGCCGCATTT	GCTGCTTAAG	CAAGGGGAAC	1800
TGGGGCTGAG	CACACACCGG	GGTGCCCCCG	GATTTTTTCT	CAAGGGCTCT	GGAGCAACGG	1860
CACCGGCCCC	TTGGGATGCA					1880

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

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GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GCGGCGGAG GAACCTCAGC AGCAGAAGCA 60
GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120
GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180
CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240
ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300
TTCTATCGGG CTTTCGGATT CTCCCCTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360
CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420
GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480
CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540
GTGGTCTACC TCGGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600
CACTTCATCG AGGGTGGACG GACTGTCAAG GAGTTCTGCC AGCAGGAGGT GGAGCCCATG 660
TGCAAGGAGA GCGACCACAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720
CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780
GGCTCCGAGC CCAAGGTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840
TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCCT CTGCCAGGCG CTAGACATGT 900
ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTTACC CCCTTCTTCC TGTCACATGA 960
CCCCCCCCCA TGTTTTATTA AAGGGGGTGC TGGTGGTGAA AAAAAAAAAA AAAAAAAAAA 1020
AAAA                                             1024

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(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2383 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

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CCCTTCATTA AAGCCCTCCT AAATATAACT CTTCTGTATC AAAGGACTTA CAAATGTCTC 60
AAGAAAGTAA TGGTGTAGCA GTGTAAGAGA AGTAAAGTCT TGCTAGGGGA AACTAATGAA 120
GCATTTTCCT CATTACACTT TTGGGTTGAT ATATTTTCATT AAGACAGAAC TAGTCTGTGT 180
TTGCTTTGCT TTTTAGTGCT TAGTCTGAGA GGCAATGCGA GAAACCAAAA GTCTTAGGAG 240
AAAAACTGCT TTCATAATTT CCAGTGTAAG CCACAAAGAA GCTTTTCTAT AAAGGCTTGA 300
AAGCTTGAAG AGGTGACAAG AGCAAGCTGT ATTCAATTAG ACAGTTCAAT AAATATGCAA 360
AAATAAAAAA ACACTTATCA ATCATGAGTA TACTGTTTGT ATTCTGGAAA AAGCAACATA 420
TTTCATGCTT TGAATATTTT CTCTTGAGAA TAGTTTTAAA GTTATTTTCT TTTGTAACAT 480
TCAAAAGTAA AACACACATA TATAATTCCA TCAAGGATTC TCTGTATGAT TAACATTCTG 540
TACAAGTCAA ACATGACCAC ATCTATATTG GAAAGAGAGC ACTGAGAAGC AACAGCAGGA 600
GAATGCATCA CCTGTGCCTG TTTGAGGATG AACAGTTTGT TTAAGTTCAG CAGATGAATG 660
TAACAATGAC CACTTGTTTC CAAATACCCA GATGTTTCTT ACTGGCTCCT CACTAATCAA 720
TAACACAAGT GCTAAGTTCT AAGTATTTAA AAAACAAAAA GACTGCAGGT GACTCCTTCT 780
CTCTGGTCCC TTTACCAAAG CTCCAAATCA CTTATGACAT TAATTACAAT ATTCTGCACT 840
CCAAAAAAT ATGCAAACAC AGGTTTGCTA AATTTTAGTT ACTCAGTGAA CCTACTAAAT 900
TTTAAAGTAG AAAAAGACT TACATTCTCA TGACACAAAC TTTAGTTTTC ACATTCACCA 960
AAACATTTTA AAATCACTCA AACATGAGAA TTGAAAATGT GTGTGCTTAT TTGGGAGAGG1020
ATTACTGCAT TTATTCTCCA GAAAAAAGG CAGACCTGAG GCATCACA ACCGGAACAT1080
TTAAATATGA TGACATGTTT CTTATCTTCT AAACCTCAAC GAAAGCTGCT TGTACAAACT1140
ATTTAATGCA TATCTGCCCC ATTAACAAG ATATTTGATG TAGCAGAGAA GCCAGAAGCT1200
GAGTCACTTC ATTTCTTTCT GTTGCCCTCCA GTTGCCAGCA TAGTTGCAAC TCGCATAAAT1260
ATATTTAATG TATCCATGTA GATACTCAGC ATCGAGTTAA TGGGATCATA TTTTGAAGT1320
CCATACATTG GTGATACTTC TGCACGCTTG ATTACTTTCT GGGTATCATA CAGAAGGAAC1380
ATGCTGAAAA GAACATAATCC ACCGTACATT GCCACTGAGT AAAGAGTGGC ACCAGCCACG1440
GGTGGTAGGT GGAAGAAACA TAGATCCCAA TGAGGACACA AAGACGAGAC CCAGGCCAC1500
TCCCAGGGGT GCACCCATGT TCAGAAACTT TTCCTGGGC GCACACATGG CCACAGTGGA1560
GAGGCCTCCC ACAATGCCAG CTGTGTACCA TGCAGCTCTG ATGAGAAGAG GACCCCTAA1620
TATTGTGAGA GGAGCCACCA CTGCACCCAT CACACCAGAA TGTAGCAACC AAGCAAGATG1680
CTTTGGGCCT GGGCTCTGGT CATATGGTAT TGATCGTACC AGCATTCCAG CTCCAACCAT1740
GGCTGCAAAG GTCACACCAA TTGTCACCCA AGAGCCTCTC ATCATGAAGT TCATGAGAAC1800
AGGCGTTCTG CTGATTGCTA TGGCAGACAA AGCTGTAAAA CCAATACTCC CTGCTAAGTA1860
CATATAGGTG GAATGAATTC TATCCTTGAC ATACTGAGGC CAAATTACAG CCTTTTCAAT1920
AGCTCCAATC TCATTAGACA GTCCCAAGCC ATAGTAGCAC AATGCTCCAA GACCAACAGC1980
AGCCCCTCCA GCAACAAACC ATCTTCCCCT CTGATCAATT TTAAATATTT TTTCCATCGA2040
TGGTTCCAAT GCTGCCTCTT TGAGTTCTTG GCCAGTTCTC CCACGCCGGA TCCCAATTCT2100
TGTTTTGGTG GCATATTCCC TGCTAGGTGT TAACAGCCAT TGATTCTTCG TGATGGAATT2160
CTTCACAACA GGGGAGGCCT TGGTGAAAGC TGGGTGGAAG ACCCTAGAAG GTAGTGTCCG2220
GAGACACACC AGCCTTGACG CCAACATGGT GGTGGTGCAC CAGGTCTACC GAGCAGATCT2280
GAAATGCTCG GTCCCCGGTC ACCTTCGCCT CGCAGTTTCC CTTCCGGGCC CCTAGCGTCG2340
GCCTCAAAGA GCACAGTTCC TCCGGCGCAC TGCATGTGCG AAC 2383

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(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3210 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

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GCAAGGCCTA CTGTCGGCTG GGAGGGGAGG TGTAGCCGGT CTTTGGGGGT AGGCGGTAGT 60
GGCGGAAGAG GTTCGGCGGC TGATGGCGGA TCAGGATCGG AAGCCTGCGT AACTTTCTCC 120
CTTGATCCGG GAGTCTTTCC ACTGGATTCA CAATGACATC CTTTCAAGAA GTCCCATTCG 180
AGACTTCCAA CTTTGCCCAT GTCATCTTTC AAAATGTGGC CAAGAGTTAC CTTCCTAATG 240
CACACCTGGA ATGTCATTAC ACCTTAACTC CATATATTCA TCCACATCCA AAAGATTGGG 300
TTGGTATATT CAAGGTTGGA TGGAGTACTG CTCGTGATTA TTACACGTTT TTATGGTCCC 360
CTATGCCTGA ACATTATGTG GAAGGATCAA CAGTCAATTG TGTACTAGCA TTCCAAGGAT 420
ATTACCTTCC AAATGATGAT GGAGAATTTT ATCAGTTCTG TTACGTTACC CATAAGGGTG 480
AAATTTCGTG AGCAAGTACA CCTTTCAGT TTCGAGCTTC TTCTCCAGTT GAAGAGCTGC 540
TTACTATGGA AGATGAAGGA AATTCTGACA TGTTAGTGGT GACCACAAA GCAGGCCTTC 600
TTGAGTTGAA AATTGAGAAA ACCATGAAAG AAAAAGAAGA ACTGTTAAAG TTAATTGCCG 660
TTCTGGAAAA AGAAACAGCA CAACTTCGAG AACAAGTTGG GAGAATGGAA AGAGAACTTA 720
ACCATGAGAA AGAAAGATGT GACCAACTGC AAGCAGAACA AAAGGGTCTT ACTGAAGTAA 780
CACAAAGCTT AAAAATGGAA AATGAAGAGT TTAAGAAGAG GTTCAGTGAT GCTACATCCA 840
AAGCCCATCA GCTTGAGGAA GATATTGTGT CAGTAACACA TAAAGCAATT GAAAAAGAAA 900
CGAATTAGA CAGTTTAAAG GACAACTCA AGAAGGCACA ACATGAAAGA GAACAACTTG 960
AATGTCAGTT GAAGACAGAG AAGGATGAAA AGGAACTTTA TAAGGTACAT TTGAAGAATA1020
CAGAAATAGA AAATACCAAG CTTATGTCAG AGGTCCAGAC TTTAAAAAAT TTAGATGGGA1080
ACAAAGAAAG CGTGATTACT CATTTCAAAG AAGAGATTGG CAGGCTGCAG TTATGTTTGG1140
CTGAAAAGGA AAATCTGCAA AGAACTTTCC TGCTTACAAC CTCAAGTAAA GAAGATACTT1200
GTTTTTTTAA GGAGCAACTT CGTAAAGCAG AGGAACAGGT TCAGGCAACT CGGCAAGAAG1260
TTGTCTTTCT GGCTAAAGAA CTCAGTGATG CTGTCAACGT ACGAGACAGA ACGATGGCAG1320
ACCTGCATAC TGCACGCTTG GAAAACGAGA AAGTGAAAAA GCAGTTAGCT GATGCAGTGG1380
CAGAACTTAA ACTAAATGCT ATGAAAAAAG ATCAGGACAA GACTGATACA CTGGAACACG1440
AACTAAGAAG AGAAGTTGAA GATCTGAAAC TCCGTCTTCA GATGGCTGCA GACCATTATA1500
AAGAAAAATT TAAGGAATGC CAAAGGCTCC AAAAACAAAT AAACAACTT TCAGATCAAT1560
CAGCTAATAA TAATAATGTC TTCACAAAGA AAACGGGGAA TCAGCAGAAA GTGAATGATG1620
CTTCAGTAAA CACAGACCCA GCCACTTCTG CCTCTACTGT AGATGTAAAG CCATCACCTT1680
CTGCAGCAGA GGCAGATTTT GACATAGTAA CAAAGGGGCA AGTCTGTGAA ATGACCAAAG1740
AAATTGCTGA CAAAACAGAA AAGTATAATA AATGTAAACA ACTCTTGCAG GATGAGAAAG1800
CAAAATGCAA TAAATATGCT GATGAACTTG CAAAATGGA GCTGAAATGG AAAGAACAAG1860
TGAAAATTGC TGAAAATGTA AAACCTGAAC TAGCTGAAGT ACAGGACAAT TATAAAGAAC1920
TTAAAAGGAG TCTAGAAAAA CCAGCAGAAA GGAAAATGGA AGATGGAGCA GATGGTGCTT1980
TTTACCCAGA TGAAATACAA AGGCCACCTG TCAGAGTCCC CTCTTGGGGA CTGGAAGACA2040
ATGTTGTCTG CAGCCAGCCT GCTCGAAACT TTAGTCGGCC TGATGGCTTA GAGGACTCTG2100
AGGATAGCAA AGAAGATGAG AATGTGCCTA CTGCTCCTGA TCCTCCAAGT CAACATTTAC2160

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GTGGGCATGG GACAGGCTTT TGCTTTGATT CCAGCTTTGA TGTTCAACAAG AAGTGTCCCC2220
TCTGTGAGTT AATGTTTCCT CTTAACTATG ATCAGAGCAA ATTTGAAGAA CATGTTGAAA2280
GTCACCTGGAA GGTGTGCCCC ATGTGCAGCG AGCAGTTCCC TCCTGACTAT GACCAGCAGG2340
TGTTTGAAAAG GCATGTGCAG ACCCATTTTG ATCAGAATGT TCTAAATTTT GACTAGTTAC2400
TTTTTATTAT GAGTTAATAT AGTTTAGCAG TAAAAA AAAA AAAAAC CACACCTAAA2460
ATAGACCACT GAGGAGACCA TAGAGCGGAT GCTTTCATGC ACCCTTTACT GCACTTTCTG2520
ACCAGGAGCT ACTTTGAGTT TGGTGTTACT AGGATCAGGG TCAGTCTTTG GCTTATCAAT2580
AAATTTTAAT CTCTGTTAAT CTTACCTGCT TTAAAAA GTTCTTGTGT GTTCGTATCT2640

TTATTTATTC CCTAGTTTGC AGAACTGTCT GAATAAAGGA TACAAGGATT ATTTCAATGT2700
TACTGCACTG AAAAACGTGT ATGTATTAGT GTGCTAGATT ATTTAGCAGA ATATTCACAA2760
GTTTCTGTTG ACCTTGTTGA TTGAGCATGA CTTACTAAATA TTATGTAATA AAAAGCATTT2820
GTCATAACAG TCTTATGAAG TAGTCTTCG AATATAGAAA GTTCTATAAT TTAGCCCATG2880
AAATGATAGG TTTTAAATTT TCAGAAATGG AGCTGCATGT AGAATGAGAT CACATGCTTT2940
TATATGTGAA ATATTGGTTT TAGCAATTAA CAGAAGGCAT ACTTTGCTAA TTTTATGGCA3000
AAATTTTAGA ATAACCTGAA TGATTATTTT TAACTATCT TGAAGTTGTA TGTATATATC3060
CTAATGGGGA AATGGGGCAA GGGATTGTCA GTATAATTGT TTTCCCGATT AAATGGTCCC3120
CATAACCAGG GGGTGTTTGT GGCATAAAAA TCCATAGGGT ATATAGCAGG ACCTTTTTTG3180
CATTTCCCTG TGGGGATTTA ATTTGGAATT 3210

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

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CCGCTTTCTC CGCCCAGCTG GAATTTTGA AGCGAGAAAA TCGACTCGCT CGGTGTTCGC 60
CCGCCGACGC CGCACGGTTG CTGGGGCTGG GCTCTTCCTC GCGGAAGTGG GGAGGAGGCG 120
GTTGCGGTTA GTGGACCGGG ACCGGTAGGG GTGCTGTTGC CATCATGGCT GACCCCGACC 180
CCCGGTACCC TCGCTCCTCG ATCGAGGACG ACTTCAACTA TGGCAGCAGC GTGGCCTCCG 240
CCACCGTGCA CATCCGAATG GCCTTTCTGA GAAAAGTCTA CAGCATTCTT TCTCTGCAGG 300
TTCTCTTAAC TACAGTGACT TCAACAGTTT TTTTATACTT TGAGTCTGTA CGGACATTTG 360
TACATGAGAG TCCTGCCTTA ATTTTGCTGT TTGCCCTCGG ATCTCTGGGT TTGATTTTTG 420
CGTTGACTTT AAACAGACAT AAGTATCCCC TTAACCTGTA CCTACTTTTT GGATTTACGC 480
TGTGGAAGC TCTGACTGTG GCAGTTGTTG TTACTTTCTA TGATGTATAT ATTATTCTGC 540
AAGCTTTCAT ACTGACTACT ACAGTATTTT TTGGTTTGAC TGTGTATACT CTACAATCTA 600
AGAAGGATTT CAGCAAATTT GGAGCAGGGC TGTGTGCTCT TTTGTGGATA TTGTGCCTGT 660
CAGGATTCTT GAAGTTTTTT TTTTATAGTG AGATAATGGA GTTGGTCTTA GCCGCTGCAG 720
GAGCCCTTCT TTTCTGTGGA TTCATCATCT ATGACACACA CTCACTGATG CATAAACTGT 780
CACCTGAAGA GTACGTATTA GCTGCCATCA GCCTCTACTT GGATATCATC AATCTATTCC 840
TGCACCTGTT ACGGTTTCTG GAAGCAGTTA ATAAAAGTA TCTCAGCTCA 900
ACTGAAGAAC AACAAAAAAA ATTTAACGAG AAAAAAGGAT TAAAGTAATT GGAAGCAGTA 960
TATAGAAACT GTTTCATTAA GTAATAAAGT TTGAAACAAT GATTAAAAAA AAAAAAAAAA1020

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(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```

TCTGTTCTGT GGACAACTGT TACTGTTCTT CCGTGGCCAA CCATGGCGGC CACCAGCCCT 60
ACCCCCGCTC CGGCCACTTT CCCTGGACAG TGCCCTCGCA GGAGTACTCA CACCCGCTCC 120
CGCCACACC CTCCGTCCCC CAGTCCCTTC CCAGCCTGGC GGTCAGAGAC TGGCTTGACG 180
CCTCCCAGCA GCCCGGCCAC CAGGATTTCT ACAGGGTGTA TGGGCAGCCG TCCACCAAAC 240
ACTACGTGAC GAGCTAACGC CACGCAGGCG GCGGGGCGCT GGGGAATCTT CCTCCCCAGC 300
CCCCGGGCTC GGGAGTTATG CATCCAGAGA CCTGCCCTTC TACCTTCCTC GCCTCCCCTC 360
TTCCTCATTC CATTGCCCCA GGTCTTTTCC TTTTGGATTT TGTTTTGGTT TTGGCTTTGT 420
TTTTGATTTT TTTTATTAT GAATCTCCTG GACGCAGAGG TGACAGTGGG AGCTGGCCTG 480
GGCCAGGACG GCAGGTGGCC CTGGAGATGG GAAAGTGTCT GTGTCGAGGC GCTGAGCTCT 540
CTCTCTGTTT CTCCTTTTTT CCTCTACTCC TTCCCCTTCA CACCCCCGTG GCTGGAAGGA 600
ACCTCGGCTT CCCTGAAAGC TTGGGGGTCC CACCCTTCTT ACCCCACCCG GGAGGAACGC 660
CCAGGGCCCC GGGCTTGTTT CTCCTCTGTG TTTCTTTTG GGCAGTTTGA TCACTGATCG 720
AGTAAGGAAT GACCTTTAGA TTGTGCGACT TTTGTTTGG TTTTAA TTTTAA 780
CCAAGAATGA TTTCTCCTGC TTCCTTCTCC TCACCATCTT CCCAGACGGA GTTCAAAGGC 840
CACTTCTCAA GCAGCTTTTG GCACCTTCAG CCTCAGAGTG GAATCTTTA AAGACAGGAC 900
CCCTATGTCC AGGAAAGGGG AAAAGGAACT TTGCCAATGA TAGTGACCAC AGCAAAAGCA 960
ATAAAATAAT AAAATAAAAA ACAATAGCAC AGCCCTTGTT GAGGTCAGCA GGGAGGAGGG1020
GCTGCCCCGA GTTGGGTCCT TGCCTGGATT TTGACACAGC AACTTCCTGT AGTGAGCACT1080
TTGTATGAAT CGTGGACTTC CTGTTCTCAA GGCGCAGGTA TTTATTCTGT ATCTGTCTAG1140
AGCACACACC AAAATCCAAC CTTCTAATAA ACATGATGGC GCAGTCCCAA AAAAAAGAAA1200
CAGAAGAAGA AAAGGG
1216

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(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2369 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CGGGCGCCCCG GGCCAGAGTC CGGCCGGAGC GGAGGAGCCC GGCCCCAGGG ACAGCTCGGC 60
 CGTCATTACT CAGATCAGCA AGGAGGAGGC TCGGGGCCCCG CTGCGGGGCA AAGGTGACCA 120
 GAAGTCAGCA GCTTCCCAGA AGCCCCGAAG CCGGGGCATC CTCCACTCAC TCTTCTGCTG 180
 TGTCTGCCGG GATGATGGGG AGGCCCTGCC TGCTCACAGC GGGGCGCCCC TGCTTGTGGA 240
 GGAGAATGGA GCCATCCCTA AGACCCAGT CCAATACCTG CTCCCTGAGG CCAAGGCCCA 300
 GGA CT CAGAC AAGATCTGCG TGGTCATCGA CCTGGACGAG ACCCTGGTGC ACAGCTCCTT 360
 CAAGCCAGTG AACACGCGG ACTTCATCAT CCCTGTGGAG ATTGATGGGG TGGTCCACCA 420
 GGTCTACGTG TTGAAGCGTC CTCACGTGGA TGAGTTCCTG CAGCGAATGG GCGAGCTCTT 480
 TGAATGTGTG CTGTTCACTG CTAGCCTCGC CAAGTACGCA GACCCAGTAG CTGACCTGCT 540
 GGACAAATGG GGGGCCTTCC GGGCCCGGCT GTTTCGAGAG TCCTGCGTCT TCCACCGGGG 600
 GAACTACGTG AAGGACCTGA GCCGGTTGGG TCGAGACCTG CGGCGGGTGC TCATCCTGGA 660
 CAATTCACCT GCCTCCTATG TCTTCCATCC AGACAATGCT GTACCGGTGG CCTCGTGGTT 720
 TGACAACATG AGTGACACAG AGCTCCACGA CCTCCTCCCC TTCTTCGAGC AACTCAGCCG 780
 TGTGGACGAC GTGTACTCAG TGCTCAGGCA GCCACGGCCA GGGAGCTAGT GAGGGTGATG 840
 GGGCCAGGAC CTGCCCCTGA CCAATGATAC CCACACCTCC TCCCAGGAAG ACTGCCCAGG 900
 CCTTTGTTAG GAAAACCCAT GGGCCGCCGC CACACTCAGT GCCATGGGGA AGCGGGCGTC 960
 TCCCCACCA GCCCCACCAG GCGGTGTAGG GGCAGCAGGC TGCACTGAGG ACCGTGAGCT1020
 CCAGGCCCCG TGTCAGTGCC TTCAAACCTC CTCCCCTATT CTCAGGGGAC CTGGGGGCC1080
 CTGCTTGCTG CTCCCTTTTT CTGTCTCTGT CCATGTGCC ATGTTTCTCT GCTGCCAAAT1140
 TGGGCCCCCTT GGCCCTTCC GTTCTGCTT CCGGGGGCA GGGTTCCTGC CTTGGACCCC1200
 CAGTCTGGGA ACGGTGGACA TCAAGTGCCT TGCATAGAGC CCCCTCTTCC CCGCCAGCT1260
 TTTCCAGGGG CACAGCTCTA GGCTGGGAGG GGAGAACCAG CCCCTCCCC TGCCCCACCT1320
 CCTCCCTTGG GACTGAGAGG GCCCTACCA ACCTTTGCCT CTGCCTTGA GGGAGGGGAG1380
 GTCTGTTACC ACTGGGGAAG GCAGCAGGAG TCTGTCTTCC AGGCCCCACA GTGCAGCTTC1440
 TCCAGGGCCG ACAGCTGAGG GCTGCTCCCT GCATCATCCA AGCAATGACC TCAGACTTCT1500
 GCCTTAACCA GCCCGGGGGC TTGGCTCCCC CAGCTCTGAG CGTGGGGGCA TAGGCAGGAC1560
 GGGGCTTGTG GTGCCATATA AATATGTACA TGTGTATATA GATTTT TAGG GGAAGGAGAG1620
 AGGGAAGGGT CAGGGTAGAG ACACCCCTCC CTTGCCCCCT TCCTGGGCCC AGAAGTTGGG1680
 GGGAGGGAGG GAAAGGATTT TTACATTTTT TAAACTGCTA TTTTCTGAAT GGAACAAGCT1740
 GGGCCAAGGG GCCCAGGCCC TGTCCTCTGT CCCTCACACC CCTTTGCTCC GTTCATTCAT1800
 TCAAAAAAAC ATTTCTTGAG CACCTTCTGT GCCCAGCATA TGCTAGGCCC ACCAGCTAAG1860
 TGTGTGTGGG GGGTCTCTAC GCCAGCTCAT CAGTGCCTCC TTGCCCATCC TTCACCGGTG1920
 CCTTTGGGGG ATCTGTAGGA GGTGGGACCT TCTGTGGGGT TTGGGGATCT CCAGGAAGCC1980

 CGACCAAGCT GTCCCCCTTCC CCTGTGCCAA CCCATCTCCT ACAGCCCCCT GCCTGATCCC2040
 CTGCTGGCTG GGGGCAGCTC CCAGGATATC CTGCCTTCCA ACTGTTTCTG AAGCCCCCTCC2100
 TCCTAACATG GCGATTCCGG AGGTCAAGGC CTTGGGCTCT CCCCAGGGTC TAACGGTTAA2160
 GGGGACCCAC ATACCAGTGC CAAGGGGGAT GTCAAGTGGT GATGTCGTTG TGCTCCCCCTC2220
 CCCCAGAGCG GGTGGGCGGG GGGTGAATAT GGTGGGCTG CATCAGGTGG CCTTCCCATT2280
 TAAGTGCTT CTCTGTGACT GAGAGCCCTA GTGTGATGAG AACTAAAGAG AAAGCCAGAC2340
 CCCTAAAAAA AAAAAAAAAA AAAAAAAAAA 2369

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 849 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

CGAAACGTGC	GCAGGCGCCG	GCCGCTGCGC	TGCAGATGGC	GGAAATGGAT	CCGGTAGCCG	60
AGTTCCCCCA	GCCTCCCGGT	GCTGCGCGCT	GGGCTGAGGC	CCTTCTGCGA	TGTTTTACCT	120
GGCTGCGGCT	GTGTCAGATT	TCTATGTTCC	TGTCTCTGAA	ATGCCTGAAC	ACAAGATCCA	180
GTCATCTGGG	GGCCCACTGC	AGATAACAAT	GAAGATGGTG	CCAAAACCTGC	TTTCTCCTTT	240
GTTTAAAGAT	TGGGCTCCCA	AAGCATTTAT	AATTCCTTT	AAGTTGGAGA	CTGACCCCGC	300
CATTGTAATT	AATCGAGCTC	GGAAGGCTTT	GGAAATTTAT	CAGCATCAAG	TGGTGGTGGC	360
TAATATCCTT	GAGTCACGAC	AGTCCTTTGT	GTTTATTGTA	ACCAAAGACT	CGGAAACCAA	420
GTTATTGCTA	TCAGAGGAAG	AAATAGAAAA	AGGCGTAGAG	ATAGAAGAGA	AGATAGTGGA	480
TAATCTTCAG	TCTCGACACA	CAGCTTTTAT	AGGTGACAGA	AACTGAAGTA	AAAAGCCCTT	540
ATAGGATCAA	AAATTGTTCA	GGGCTCTTAG	AGATGGTGAA	AACTACAAA	AAAACCATGG	600
CTTTCATATG	GACAGATAAA	ATGAAAGAGA	GGGAAAAGGC	AGTGGTGTGT	AGGCAAATAT	660
GGTTTGGCAT	TTGTCTTTTA	ATGACACCTG	ATATGATGTC	ATTTTGATTT	TGAAATTGAA	720
CACTAGAACT	GTTAATCACC	TTTAAAAAGG	AAGAGCTTAT	TGGGGATTAT	ATATTCCTTA	780
AAAATATACA	TGGGGGCCTG	AATGTCAGCC	ATCTGTATAC	TGTGGGGAAA	AGGGGTTTGG	840
GTGCAATTC						849

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

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CCTTACCGGC AGGGCTGCCC AGGAGCTGCA GGACAAGCAC CAGGAGCCCC TCCGGGTAGC 60
TACTACCCTG GACTCCCCTC TGGAAGTCCA GGAGGACCAT ATGGCGGTGC AGCTCCCGGG 120
GGCCCCTATG GTCAGCCACC TCCAAGTTCC TACGGTGCCC AGCAGCCTGG GCTTTATGGA 180
CAGGGTGGCG CCCCTCCCAA TGTGGATCCT GAGGCCTACT CCTGGTTCCA GTCGGTGGAC 240
TCAGATCACA GTGGCTATAT CTCCATGAAG GAGCTAAAGC AGGCCCTGGT CAACTGCAAT 300
TGGTCTTCAT TCAATGATGA GACCTGCCTC ATGATGATAA ACATGTTTGA CAAGACCAAG 360
TCAGGCCGCA TCGATGTCTA CGGCTTCTCA GCCCTGTGGA AATTCATCCA GCAGTGGAAG 420
AACCTCTTCC AGCAGTATGA CCGGGACCGC TCGGGCTCCA TTAGCTACAC AGAGCTGCAG 480
CAAGCTCTGT CCCAAATGGG CTACAACCTG AGCCCCCAGT TCACCCAGCT TCTGGTCTCC 540
CGCTACTGCC CACGCTCTGC CAATCCTGCC ATGCAGCTTG ACCGCTTCAT CCAGGTGTGC 600
ACCCAGCTGC AGGTGCTGAC AGAGGCCTTC CGGGAGAAGG ACACAGCTGT ACAAGGCAAC 660
ATCCGGCTCA GCTTCGAGGA CTTCGTCACC ATGACAGCTT CTCGGATGCT ATGACCCAAC 720
CATCTGTGGA GAGTGGAGTG CACCAGGGAC CTTCTCTGGC TTCTTAGAGT GAGAGAAGTA 780
TGTGGACATC TCTTCTTTTC CTGTCCCTCT AGAAGAACAT TCTCCCTTGC TTGATGCAAC 840
ACTGTTCCAA AAGAGGGTGG AGAGTCCTGC ATCATAGCCA CCAAATAGTG AGGACCGGGG 900
CTGAGGCCAC ACAGATAGGG GCCTGATGGA GGAGAGGATA GAAGTTGAAT GTCCTGATGG 960
CCATGAGCAG TTGAGTGGCA CAGCCTGGCA CCAGGAGCAG GTCCTTGTA TGGAGTTAGT1020
GTCCAGTCAG CTGAGCTCCA CCCTGATGCC AGTGGTGAGT GTTCATCGGC CTGTTACCGT1080
TAGTACCTGT GTTCCCTCAC CAGGCCATCC TGTCAAACGA GCCCATTTTC TCCAAAGTGG1140
AATCTGACCA AGCATGAGAG AGATCTGTCT ATGGGACCAG TGGCTTGGAT TCTGCCACAC1200
CCATAAATCC TTGTGTGTTA ACTTCTAGCT GCCTGGGGCT GGCCCTGCTC AGACAAATCT1260
GCTCCCTGGG CATCTTTGGC CAGGCTTCTG CCCTCTGCAG CTGGGACCCC TCACTTGCCT1320
GCCATGCTCT GTCGGCTTC AGTCTCCAGG AGACAGTGGT CACCTCTCCC TGCCAATACT1380
TTTTTTAATT TGCATTTTTT TTCATTTGGG GCCAAAAGTC CAGTGAAATT GTAAGCTTCA1440
ATAAAAGGAT GAAACTCTGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA1500
AA

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1502

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1892 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

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CATAATTTCGC TTTAGAGTCA TTTTCCAGC AATGTTTAAA TTA CTTTCTC ATTCTTTTAG 60
TGTATTC AAC ATTGCTGCC TCTTCCTGCA GTTGATGTAA TTGCTTTGTT TGCAATAGCA 120
CAAGCTGCAT TATTCAGCTC AGGACTGTGA TAACTTGCTG CCAGCCCCAC TCAACTTTCA 180
GTTGGCTCTG TGTCAGTTTT CCACCTCAGTG TTAAC TACTT GTTACTGCCA TGCTGCTTGC 240
CCTCCCTTGA AGTGTCTATA AGCTCATCAC AGCCTAGAGT TAAGTAAAGT CAATTCACAG 300
AAGCACAATT TTGCCCTTTG CGAGACATTG TTGCCTCTAT CTAGTCCTAC AAGTAGGGTT 360
TTGCATACTG TGTTTGCCCC TAGGGTTGTC AGTGCATCAG AAATACTTCT AAATAGTGGT 420
AAAAATGCAC ATGGTTAATG CACATGTTAC TTTTAAATCA TTAGGATATC CCTCACCTGT 480
TCCTGATGAA TAAAAAGTGT GTTAAAGACC AAAATTCCTG GCATAATAAT CAGCTACATA 540
CAAATCACAT ATAGTTTAAAT CTTTTTTTAAAT GGAAAAAATA TCATGTTTAA AATGGCAAAA 600
GCCCATCTTA TACACTTTTA TATAGCTGCA AAAAATTTAT ATCTGTACAG ATCTAACACT 660
ACGACACTCA GTATTCATTT TATTGAAGCA TGCAAGTAAA GCACTTTTTT TAATTTATAT 720
AGAGGTATCT AATTAACACA GCACATTGTA CTAATGACTA GGAGTAGCAG CTTTTTCTTC 780
TCTCCCTCTA TGAATTCTTA TAATGTCCCT TTTTCTGTAA GTTTTTGAGA GGCAATTGGC 840
AATTTAGGAG GCAGCAGGGT CTGTTTTTGGT CAAATCTTGA ATTTTCGTTGT TGCACTCTAG 900
TGACTGATCT TTGGGAATGT CTTGTCTTTG CATGGGGCTC ATAGAGATGT GTGCAGACTT 960
GCTTATTGTG GTTAGTGTGT ATCAGGAACA CACACACAGG TGTTCTGACC AGCTCAGGCT 1020
TGCCACAGTG AGCAACTCTG TGGCTAGCAA AAGAGAAGTT TATTTGTGCC CAGCCATTGG 1080
TCACCTTGGG TGATGCACCA GATAGCAGGC AGATGTTGGT TCATTGGCCT TCGTCTCTTT 1140
TCCTCCTAAA ATAATATTGG CTTTACCATC TTAAC TACAGC TGTGGGTTTT TTGTGGGTTC 1200
TTGTTTGT TTGTCATGA ATTGTCATCT TTGGTGT TTTAACCCCC AGCCCTCAA 1260
AAAAATAAGG CCTCCAGGTA TCAAGATCTC ATATTAGGAT TTTCTGTCCT TAATTTTTTG 1320
AGCAAAATCT GGAAAATGTG AAAGCATATT TAGATTTTAT ATACTATCTG AAATGTGATT 1380
TGTTAAGATT CTAAATTTG GGCCTCTTAG AATAATTTTG AATGAGATCT ACCGACTCAC 1440
TTGTGAGAAT ATTTTTCACA GATTATCTTT GGGCCTTTTC ATTAGAAAGC TGTTTGTGTT 1500
TCCCCCTGTT GGTACATTTG GTTACCTCAT TTTGCCGTTT CAGATTGTGA AAGCTCACAG 1560
GGGTGTTTTT TGGAATCATT TGCTGAGTCA TTTTCTCAA TCATATTCCA TTGTATCAGT 1620
TAACATATAG TTTTAAATGT ATGTATTATA AATATCTGTA ACCAAATCAT TTGAAGGCTT 1680
GATAAATTTT TAACAAAGTT TGTACATTTT TTATGAAAGT TACTAGTAAT GCTTTACTAA 1740
GTAGTGCAAT GAATTTTTAT TTTTAATCCC TGTGCCCAAT TTTGGAGTTG AGAGGGTTGT 1800
TGGTAATAAA TGTATGATGT ACACTTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 1892

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(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

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CAGGAGTGCG GACCAGCGGG TGCCTGTAGT GGGTGGGAATT GGGGTCTGCA CTTGCCCCCTC 60
CGCCCCCAGG TGGGAGTCAC CTGGAGCGTG AAGGGACGTG TCTCATCCCC AGTGTGTCGG 120
ACCCTGGAGA CACAGCCGCA GAGCAGCCCC TTCTCATGCA TGGACCTCAC CTACGTCAGC 180
CTGCTACTCC AGGAGTTCGG CTTTCCCAGG AGCAAAGTGC TGAAGCTCAC TCGGAAAATT 240
GACAATGTTG AGACCAGCTG GGCTCTGGGG GCCATTTTTC ATTACATCGA CTCCCTGAAC 300
AGACAGAAGA GTCCAGCCTC ATAGTGGCCG AGCCATCCCT GTCCCCGTCA GCAGTGTCTG 360
TGTGTCTGCA TAAACCTCC TGTCCTGGAC GTGACTTCAT CCTGAGGAGC CACAGCACAG 420
GCCGTGCTGG CACTTTCTGC AACTGGCTC TGGGACTTGC AGAAGGCCTG GTGCTGCCCT 480
GGCATCAGCC TCTTCCAGTC ACATCTGGCC AGAGGGCTGT CTGGACCTGG GCCCTGCTCA 540
ATGCCACCTG TCTGCCTGGG CTCCAAGTGG GCAGGACCAG GACAGAACCA CAGGCACACA 600
CTGAGGGGGC AGTGTGGCTC CCTGCCTGTC CCATCCCCAT GCCCCGTCCG CGGGGCTGTG 660
GCTGCTGCTG TGCATGTCCC TGCATGGGA GTCTTGTCTC CCAGCCTGTC AGTTTCCTCC 720
CCAGGGCAGA GCTCCCCTTC CTGCNAGAGT CTGGGAGGCG GTGCAGGCTG TCCTGGCTGC 780
TCTGGGGAAG CCGAGGGACA GCCATAACAC CCCCAGGACA GTAGGTCTGG GCGGCACCAC 840
TGGGAACCTC GGACTTGAGT GTGTTGCCT CTTCTTGGG TATGAATGTG TGAGTTCACC 900
CAGAGGCCTG CTCTCCTCAC ACATTGTGTG GTTTGGGGTT AATGATGGAG GGAGACACCT 960
CCTCATAGAC GGCAGGTGCC CACCTTTCAG GGAGTCTCCC AGCATGGGCG GATGCCGGGC1020
ATGAGCTGCT GTAAACTATT TGTGGCTGTG CTGCTTGAGT GACGTCTCTG TCGTGTGGGT1080
GCCAAGTGCT TGTGTAGAAA CTGTGTTCTG AGCCCCCTTT TCTGGACACC AACTGTGTCC1140
TGTGAATGTA TCGCTACTGT GAGCTGTTCC CGCCTAGCCA GGGCCATGTC TTAGGTGCAG1200
CTGTGCCACG GGTGAGCTGA GCCACAGTCC CAGAACCAAG CTCTCGGTGT CTCGGGCCAC1260
CATCCGCCCA CCTCGGGCTG ACCCCACCTC CTCCATGGAC AGTGTGAGCC CCGGGCCGTG1320
CATCCTGCTC AGTGTGGCGT CAGTGTGCGG GCTGAGCCCC TTGAGCTGCT TCAGTGAATG1380
TACAGTGCCC GGCACGAGCT GAACCTCATG TGTTCCACTC CCAATAAAAG GTTGACAGGG1440
AAAAAAAAAA AAAAAAACT CGAGCGGAAC GAGCTCACTT TCTTCTAGCT GAGCTTTAAA1500
ACATTAGAGC TTAAATTTTC AG
1522

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(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```

GAGAAAAATGG AGGCCTTTGG GGAAGGGGCA GGGTGGGAGG ATTTCTTCTC CACACAGACC 60
TTAACCTTCC AATCTATTCT GCAGATGAAG AATGCCGACT ACTTCTCCAA CTATGTCACA 120
GAGGACTTTA CCACCTACAT TAACAGGAAG CGGAAAAACA ATTGCCATGG CAACCACATT 180
GAGATGCAGG CCATGGCAGA GATGTACAAC CGTCTGTGG AGGTGTACCA GTACAGCACA 240
GAACCCATCA ACACATTCCA TGGGATACAT CAAAACGAGG ACGAACCCAT TCGTGTTAGC 300
TACCATCGGA ATATCCACTA TAATTCAGTG GTGAATCCTA ACAAGGCCAC CATTGGTGTG 360
GGGCTGGGCC TGCCATCATT CAAACCAGGG TTTGCAGAGC AGTCTCTGAT GAAGAATGCC 420
ATAAAAAACAT CGGAGGAGTC ATGGATTGAA CAGCAGATGC TAGAAGACAA GAAACGGGCC 480
ACAGACTGGG AGGCCACAAA TGAAGCCATC GAGGAGCAGG TGGCTCGGGA ATCCTACCTG 540
CAGTGGTTGC GGGATCAGGA GAAACAGGCT CGCCAGGTCC GAGGCCCCAG CCAGCCCCCG 600
AAAGCCAGCG CCACATGCAG TTCGGCCACA GCAGCAGCCT CCAGTGGCCT GGAGGAGTGG 660
ACTAGCCGGT CCCC GCGGCA GGGAGTTCAG CCTCGTCACC TGAGCACCTT GAGCTGCATG 720
CTGAATTGGG CATGAAGCCC CCTTCCCCAG GCACTGTTTT AGCTCTTGCC AAACCTCCTT 780
CGCCCTGTGC GCCAGGTACA AGCAGTCAGT TCTCGGCAGG GGCCGACCGG GCAACTTCCC 840
CCCTTGTGTC CCTCTACCCT GCTTTGGAGT GCCGGGCCCT CATTTCAGCAG ATGTCCCCCT 900
CTGCCTTTGG TCTGAATGAC TGGGATGATG ATGAGATCCT AGCTTCGGTG CTGGCAGTGT 960
CCCAACAGGA ATACCTAGAC AGTATGAAGA AAAACAAAGT GCACAGAGAC CCGCCCCCAG 1020
ACAAGAGTTG ATGGAGACCC AGGGATTGGA CACCATCTCC CAACCCCAGT ACTCCTGCTC 1080
TCCGGTGCCA CCTCACCTTC TTTGGCTTCT TCCCTCTTGC CTCCTTCTGT TCTTTCTGCT 1140
CTCCCCTCTT TTCCCTCCTC CTCACCTCCC TCTGGCTAGC CCACCCCTGC ACTCTCTCTC 1200
ATTGCCGCTG CCACTATCAC CTGTCTCTCT GCCAGCTGAT GTGCCCTGTT GCCCCCACC 1260
CCATCCCGCA CAGAACCATC CCTGCATTCC ACAGGGGACT CGGGCAAGGG TGCCGAAGAT 1320
AGACAAGAGG CACACAGAGA CAGACCAACT GGCAGCCAGG CAGCCCCAGA GGAGAGAGAC 1380
ATTCAGACAG AGGAAAGTCT CCCTGCCCCCT CATTCCTTCC AAGATGAGAA AAAGTTGCCG 1440
CCACCCCCCG AACTGATGC CAGGGAGGTG GGAGGAAGAA GTGGGAAATT TCCCTTCCCA 1500
GTACCCCCAA GAACGTCTGA GCCTTCAATG TTGAATTTTT TCTTTATTAA AATTACTTTT 1560
ATCTTATAAA ATCAACTAAT CAAAATGAT ATAGACGACA GCACTGGCTC TGTGAAGGTG 1620
GCATCTTTCT GGGCAGGCAG GCCATGGGGC ATGGAGGAGG GTGCAAAGAT ATGGGTGCT 1680
GTCTTCTGGC CTCCAGCTGC ATGGAGGCCG GCCCAGGGTC TAGGGTGTGC ACTGGGCAAG 1740
GGCAGGGCGG CAGGTGTCAG GCCGGCTTGG ACAATGAAAC CCTGACCTTG CTGCATTCTC 1800
TTTGCTTCCA CCACCACTAG CTTCTTTTGA ATCTTGGGGT GGGGGTCATC TTTGGGGATT 1860

ATGGCTGCCA CCCGGGATTT GAGTGTAGGG AGTGTGGGAG CAGCCTTGGC AGAAGGGGCA 1920
CCCGTGCCCT GCAGGTGTTG ACAAGATCCG CCATCTGTAA TGTCTTGGC ACAATAAAAC 1980
CAAATGTCAG TTTCAAAAAA AAAAAAAAAA AAAGAC

```

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 765 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCGGATTCCG	CCCCGCCCCG	TGCGATCCGG	TTCCGCTCCC	CACAACCCGC	TCTGTGGCGG	60
GGCTTCCGGT	CGGGAGGGTC	CGCCAGCTCT	CGCGTCCTTT	GCTGGGTCCA	GACACCGGTT	120
CCGTTGCAAA	CATTTTTTAA	GGGCTGGTTA	TTCTTCCTGA	AATGAGTTTG	GTGATTAGAA	180
ATCTGCAGCG	AGTCATCCCC	ATCAGGAGAG	CGCCACTTCG	CAGTAAGATC	GAGATTGTAA	240
GGAGGATTTT	AGGAGTGCAG	AAATTTGACC	TGGGGATCAT	CTGTGTTGAC	AACAAGAATA	300
TTCAGCACAT	TAATAGAATC	TACAGAGATA	GAAATGTCCC	AACCGATGTG	CTTTCTTTTC	360
CATTTTCATG	GCATCTGAAA	GCAGGTGAAT	TTCCCCAGCC	TGATTTTCCA	GATGACTACA	420
ATTTGGGAGA	CATTTTCCTA	GGAGTGGAGT	ATATCTTCCA	TCAGTGTAAG	GAAAATGAAG	480
ATTACAATGA	CGTCCTGACT	GTGACGGCCA	CCCACGGACT	CTGTCACTTG	CTGGGATTCA	540
CACACGGCAC	GGAGGCAGAG	TGGCAGCAGA	TGTTCCAGAA	GGAGAAGGCG	GTGCTGGACG	600
AGCTGGGCCG	ACGCACGGGG	ACCCGGCTGC	AAGCCCTGAC	CCGGGGCCTC	FTCGGAGGGA	660
GCTGAGGGCC	GCGTTCCTTC	TGAAAGCGGG	ACGCGGGAGG	GGTGGAGGCT	GCGGGGAGCC	720
GGGGTCGCAC	ACAAATAAAT	AACGAATGAA	CGTAAAAAAA	AAAAA		765

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1611 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

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CTGCTTGGCG CGACGCTCTA GCGGTTACCG CTGCGGGCTG GCTGGACCGT AGTGGGGCTG 60
CGCGGCTGCC ACGGAGCTAG AGGGGTTAAA AACTAATATT TATATGACAG AAGAAAAAGA 120
TGTCATTCCG TAAAGTAAAC ATCATCATCT TGGTCCTGGC TGTTGCTCTC TTCTTACTGG 180
TTTTGCACCA TAACTTCCTC AGCTTGAGCA GTTTGTTAAG GAATGAGGTT ACAGATTCAG 240
GAATTGTAGG GCCTCAACCT ATAGACTTTG TCCCAAATGC TCTCCGACAT GCAGTAGATG 300
GGAGACAAGA GGAGATTCCCT GTGGTCATCG CTGCATCTGA AGACAGGCTT GGGGGGGCCA 360
TTGCAGCTAT AAACAGCATT CAGCACAACA CTCGCTCCAA TGTGATTTTC TACATTGTTA 420
CTCTCAACAA TACAGCAGAC CATCTCCGGT CCTGGCTCAA CAGTGATTCC CTGAAAAGCA 480
TCAGATACAA AATTGTCAAT TTTGACCCTA AACTTTTGGA AGGAAAAGTA AAGGAGGATC 540
CTGACCAGGG GGAATCCATG AAACCTTTAA CCTTTGCAAG GTTCTACTTG CCAATTCTGG 600
TTCCCAGCGC AAAGAAGGCC ATATACATGG ATGATGATGT AATTGTGCAA GGTGATATTC 660
TTGCCCTTTA CAATACAGCA CTGAAGCCAG GACATGCAGC TGCATTTTCA GAAGATTGTG 720
ATTACGCCTC TACTAAAAGT GTCATCCGTG GAGCAGGAAA CCAGTACAAT TACATTGGCT 780
ATCTTGAATA TAAAAAGGAA AGAATTTCGT AGCTTTCCAT GAAAGCCAGC ACTTGCTCAT 840
TTAATCCTGG AGTTTTTGTG GCAAACCTGA CGGAATGGAA ACGACAGAAT ATAACCTAAC 900
AACTGGAAAA ATGGATGAAA CTCAATGTAG AAGAGGGACT GTATAGCAGA ACCCTGGCTG 960
GTAGCATCAC AACACCTCCT CTGCTTATCG TATTTTATCA ACAGCACTCT ACCATCGATC 1020
CTATGTGGAA TGTCCGCCAC CTTGGTTCCA GTGCTGGAAA ACGATATTCA CCTCAGTTTG 1080
TAAAGGCTGC CAAGTTACTC CATTGGAATG GACATTTGAA GCCATGGGGA AGGACTGCTT 1140
CATATACTGA TGTTTGGGAA AAATGGTATA TTCCAGACCC AACAGGCAA TTCAACCTAA 1200
TCCGAAGATA TACCGAGATC TCAAACATAA AGTGAAACAG AATTTGAACT GTAAGCAAGC 1260
ATTTCTCAGG AAGTCCTGGA AGATAGCATG CGTGGGAAGT AACAGTTGCT AGGCTTCAAT 1320
GCCTATCGGT AGCAAGCCAT GGAAAAAGAT GTGTCAGCTA GGTAAAGATG ACAAAC TGCC 1380
CTGTCTGGCA GTCAGCTTCC CAGACAGACT ATAGACTATA AATATGTCTC CATCTGCCTT 1440
ACCAAGTGTT TTCTTACTAC AATGCTGAAT GACTGGAAAG AAGAACTGAT ATGGCTAGTT 1500
CAGCTAGCTG GTACAGATAA TTCAAACTG CTGTTGGTTT TAATTTTGTA ACCTGTGGCC 1560
TGATCTGTAA ATAAACTTA CATTTTTC AA AAAAAAAGA T 1611

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(2) INFORMATION ON SEQ ID NO. 231:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

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GGTGTGGTCC TCAGGGGGCT GTAGGGTGGG AGGTATGGCT TCAGGTGCCA AGTTGGCGGG 60
AACGGCAGCG AGGAGGCCTG GGGGGCACTT CGGGCGCCGC AACAGCAGGT ATCCCAATAG 120
CTCCAAAACC TATCACGACA GCCATTTGTC TCTTTCCCCT TTCCTTGTCC CTCCTTTTGG 180
GGGGTGGGGG AGGAATCACG GGAGCCAAAG GTACTGTGAA GTTCCTAAAC ATGTCTCTTC 240
CACTCTTTGT CTAAACTTTG TAACGTAGAT GCAGCTGACT TTGCCTGTAG CCTCATAGAA 300
CCCATCCCAT GGCTGCAGTG GAAGCTTGCG GTGGCTCTCC AGTGACCAGA GGCATAGTGA 360
GGTCCCAGGG AGGCTCCCTC TGTCTTGCAA CAGTTATTTG TGATCTTTTT CTATGTGCCT 420
ATTGTCACAA CAGAGTCCGG CAGCGTCTTC TCTTGAGGGA GCAATTTGGA GAAGAGCTGG 480
AACCCAGACT CGCGCCCTGG ATGCCATCCT TTATCATCCA CAGCAATCCC ATCTGGTTGG 540
GAGCACTGCT CTGGGTCTCA CACTGCCCCC CCTCTATCCT AGGGAGCCTG AGGCCAGGG 600
GTGGAAGAT CCAGTTGCGG GTGGGGGGTA GTGAACCGTG CAGGATAATG AAAGCAACTT 660
GCTTTGGAAA TGACCTACCG CTACCCGTTG TCTGAGACTG AGATTATCTC AGACTGTCTT 720
CTGGCTTCTG CCAAACACT CCCTTAACAG AAAGCACCGA GGGGATGGGG GTAGGGGGGT 780
TGGGGAGAGT GAGGCTTGAG TGTGAAGGAA GTCTCATATA TGCAGAGCTG AAATCTCCCT 840
CTTTGTATGT CCACACTTTT GTCTTGTTCT CTAGACTGAT TCTTGCTATT CCAAATCCTC 900
TTCCACGTTG ACAGCCCTTC AGATATTTCA AACTCCTCT CAGCATCCTC CACTTCCCCC 960
ATCTCTCCAA GCTGAACCTG GTTCACAGGG TGGGATTGTG TATGTGCATG CAGGAGGTGG1020
GGGTGGACAG TGCCCTGGGC TGGAATCCCC CTTAGTTCTA AGTGCCCTCCT TGCCCGCAGC1080
TTCGAGAGCT GTGCCAGGA GTGAACAACC AGCCCTACCT CTGTGAGAGT GGTCACCTGCT1140
GCGGGGAGAC TGGCTGCTGC ACCTACTACT ATGAGCTCTG GTGGTTCTGG CTGCTCTGGA1200
CTGTCCTCAT CCTCTTTAGC TGCTGTTGCG CCTTCCGCCA CCGACGAGCT AAATCAGGC1260
TGCAACAACA GCAGCGGCAG GTGGAAATCA ACTTGTGGC CTATCATGGG GCATGCCATG1320
GGGCTGGTCC TTTCCCTACC GTTCACTGC TTGACCTTCG CTCCTCAGC ACCTTCAAGC1380
CCCCAGCCTA CGAGGATGTG GTTACC GCCG CAGGCACAAC GAGCCCCCCC TTATACTGTG1440
GCCCCAAGGC GCCCCTTGAG GTTGTTCAT GTG

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(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2503 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

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GAAACATGCA ACTGAACAGG AAAAAACTGA AGAGGGATTA GGCCCTAATG TAAAAGGCAT 60
TGTCACCATG TTGATGCTGA TGCTATTGAT GATGTTTGCG GTCCACTGTA CCTGGGTCAC 120
AAGCAATGCC TACTCTAGTC CAAGTGTAGT CCTGGCCTCA TACAATCATG ATGGCACCAG 180
GAATATCTTA GATGATTTTA GAGAAGCTTA CTTTGGGCTA AGGCAAAATA CAGATGAACA 240
TGCACGAGTA ATGTCTTGGT GGGATTATGG CTATCAGATA GCTGGAATGG CTAATAGAAC 300
TACGTTGGTG GATAATAACA CCTGGAATAA CAGCCACATA GCACTGGTGG GAAAAGCTAT 360
GTCTTCTAAT GAAACAGCAG CCTATAAAAT CATGAGGACT CTAGATGTAG ATTATGTTTT 420
GGTTATTTTT GGAGGGGTTA TTGGCTATTC TGGTGATGAT ATCAACAAAT TTCTCTGGAT 480
GGTTAGGATA GCTGAAGGAG AACATCCCAA AGACATTCGG GAAAGTGAAT ATTTTACCCC 540
ACAGGGAGAA TTCCGTGTAG ACAAAGCAGG ATCCCCTACT TTGTTGAATT GCCTTATGTA 600
TAAAATGTCA TACTACAGAT TTGGAGAAAT GCAGCTGGAT TTTCGTACAC CCCAGGTTT 660
TGACCGAACA CGTAATGCTG AGATTGGAAA TAAGGACATT AAATTCAAAC ATTTGGAAGA 720
AGCCTTTACA TCAGAACACT GGCTTGTTAG GATATATAAA GTAAAAGCAC CTGATAACAG 780
GGAGACATTA GATCACAAC CTGAGTCAC CAACATTTTC CCAAACAGA AGTATTTGTC 840
AAAGAAGACT ACCAAAAGGA AGCGTGGCTA CATTAAAAAT AAGCTGGTTT TTAAGAAAGG 900
CAAGAAAATA TCTAAGAAGA CTGTTTAAAT GCATGTTCT GGTTCCTAAC TTGAAGCAGT 960
TGTCCTTGTG AGAACCGGTC TTTGCCTTTA GCTCATGTCG TGTTTCACAG CAAAGAGGGT 1020
ACAGAACCAT CACTGGTCCA GGTAAATGTA CAAAATTTTC TGGCAATGCC TGATTAAAAA 1080
AATAAAATTG GCTTGTTGAG AACAGCTGTT TTCGATTTCT AATGTGAAGC AAGACAGAGC 1140
ACTGCTGTAA ATGTCTAGCA GCAGATTTTT TTTTATTGG TACATATTAT CCTTCAAATC 1200
TGAGAATTTG GACTAACTGC ACCAAGAAGC CCTCTAATTT GGTCCCTGGC ACATGCATAC 1260
TTGTCAATGT TTTTATTCTT TTACAAGACC TGCATTTTAT TTGAATTACC CGAATAGCAA 1320
TATGTAAAT ACAAGTGACA AAATGTGATG AGAGCTTCTT GAACCGGTAA ACTAGTACAG 1380
GTCTGAGAAA GACATATTAG AAGAATCATT ATACTTCCTT GAATTATATT TATTTTCATG 1440
TTTCTCTAAT GCAAAGAATG TTTCATCAAA TGTATATTTT CTGTTGCTTA CTGTTTGCTC 1500
TGAGAAGAAG CTGCTGTTTC AAAGATGGAC CTCTGAGTAG CTAATTGATT CAAGTAGTTT 1560
TTTTATGTTG ACACATTATT ACTGCTGTTA GCAGTCGTTT TCACCAGGTA CTTACAGAGC 1620
AGATTTTATA CATCTTAC TCAAGGGCTA AATTATATTT TTTTGGAAAT CATGGCAACT 1680
ACACAGGATG TTGCTTACCA GGACGGAGTT TTGGTATCTT AGTACTGAAG TTAGCACTAT 1740
GTTTACATGC AAAAGATTAA GGAAAAAACC CTTAAAGTGG ACAGGTATCC AAAGTTCATT 1800
TTCTGTGACT CATCAAAGTG ACAAAGACT TGTAACAAC TTGCCTGGAC TTTTTCATT 1860
TTACAACAGT TCATCCATTC ACAATGATTT TGTTCTCTGC TCCATATTTT TTAATCCCTT 1920

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AAGCATTGTA TGAAACACTC TTTAGTGCTA TATGCATTTT CTTACTTTTG TTAAAAATGT1980
 GACAATTGTC AAAAAATGCA CTAAAATGTA AATGGAGATT GAACAAGTTC ACTTTCAGC2040
 TTATAGGCAA CTTTATACAG ACTTGAACAT TTTCTCCAGT TGTTTAGTAA AAGTGAAAGA2100
 GAAAGGGTTT TTCCTGCCAC AGGATATAAC TTTTTTTTAT ATAACAAGCA TAACACACCA2160
 CTGCTTTTGG TGGAAAAGTG CAGAATAGTA TGTACCTTTT ATGAAGAAAA ATGTAATTTA2220
 CAATATTCAG TGAGAATGTT ACTGCTGATT TTCTTTTCCA AGGTGTAGAA TATTCTTTGA2280
 TTTATAGAAT TCATTTTTGA CCCAGATGAT GGTCCTTTA CAGAACAATA AAATGGCTGA2340
 ACATTTTCAC AAATAGAGTG TAACGAAGTC TGGATTTCTG ATACCTTGTC ATTTGGGGGA2400

TTTTATTTTA CTTTGTGCT TTAAAATTCA ATGCAGAGAA GTTGTGACT GTAGGGGAAA2460
 TAAAGTTAAT TCAAATTTTG AAAAAAAAAA AAAAAAGTCG ACG 2503

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

AAGCAACCTC GTTTATGTCT TATCTTTGCA TTTTCCTGTA TTCAGCTATT TTCTTAAAGG 60
 AAGGCCCAGG TCTGTATTAT CCTACTGCCA CATAGGAAGT AAAATGAGTA CTCACAGCCT 120
 TGCGCCTAAT CACTGAACAC AGCTTTTAGT AATGTTTTAC ACAAGAACAG GATATTGGCA 180
 ACTCAACTGT TAAGCCTTTC TGTGATTATT CTTCCCTGAG ATCACTCTGA TGTCACCACT 240
 GTAATTTGAG CCTGGAGCTT TTGTTACACAC TTAAATAGC AGTCCCAGAA TGATTTCACT 300
 ACAGACTCTC TGGAAAGCCT GGGAGCTGAA TTCCGGAAGA TCCCCACATC GATGAAAGCA 360
 AAGCGAAGCA CCAAGCCATC ATCATGTCCA CGTCGCTACG AGTCAGCCCA TCCATCCATG 420
 GCTACCACTT CGACACAGCC TCTCGTAAGA AAGCCGTGGG CAACATCTTT GAAAACACAG 480
 ACCAAGAATC ACTAGAAAGG CTCTTCAGAA ACTCTGGAGA CAAGAAAGCA GAGGAGAGAG 540
 CCAAGATCAT TTTTGCCATA GATCAAGATG TGGAGGAGAA AACGCGTGCC CTGATGGCCT 600
 TGAAGAAGAG GACAAAAGAC AAGCTTTTCC AGTTTCTGAA ACTGCGGAAA TATTCCATCA 660
 AAGTTCACTG AAGAGAAGAG GATGGATAAG GACGTTATCC AAGAATGGAC ATTCAAAGAC 720
 CAAGTGAGTT TGTGAGATTC TAACAGATGC AGCATTTTGC TGCTACCTTA CAAGCTTCTC 780
 TTCTGTCAGG ACTCCAGAGG CTGGAAAGGG ACCGGGACTG GAAAGGGACC AGGACTGAAC 840
 AGACTGGTTA CAAAGACTCC AAACAATTTT ATGCCCTGTG CTGTTACAGA GGAGAACAAA 900
 ATGCTTTTCA CAAGGATTTG AAAACTCTTC CGTCCCTGCA GGAAAGGATT GATGCTGATA 960
 GAAGAGCCTG GACAGATGTA ATGAGAACTA AAGAAAACAG ATGGCTGGAG ATGACATTTA1020
 TCCAGGGTCA CTTTGTGAGG CCCTAGGACT TAAATCGAAG TTGAACTTTT TTTTTTTTTT1080

AACCAAATAG ATAGGGGAGG GGAGGAGGGA GAGGGAGGAC AGGGAGAGAA AATACCATGC1140
 ATAAATTGTT TACTGAATTT TTATATCTGA GTGTTCAAAA TATTTCCAAG CCTGAGTATT1200
 GTCTATTGGT ATAGATTTTT AGAAATCAAT AATTGATTAT TTATTTGCAC TTATTACAAT1260
 GCCTGAAAAA GTGCACCACA TGGATGTTAA GTAGAAATTC AAGAAAGTAA GATGTCTTCA1320
 GCAACTCAGT AAAACCTTAC GCCACCTTTT GGTTTGTAAG AGGTTTTTTA TACATTTCAA1380
 ACAGGTTGCA CAAAAGTTAA AATAATGGGG TCTTTTATAA ATCCAAAGTA CTGTGAAAAC1440
 ATTTTACATA TTTTFTAAT CTTCTGACTA ATGCTAAAAC GTAATCTAAT TAAATTTTCAT1500

ACAGTTACTG CAGTAAGCAT TAGGAAGTGA ATATGATATA CAAAATAGTT TATAAAGACT1560
 CTATAGTTTC TATAATTTAT TTTACTGGCA AATGTCATGC AACATAATA AATTATTGTA1620
 AACTTTGTGA AAAATAGTCT GTGATGCTTG GTCTCAAAGG AAAAAATAAG ATGGTAAATG1680
 TTGATATTTA CAAACTTTTC TAAAGATGTG TCTCTAACAA TAAAAGTTAA TTTTAGAGTA1740
 AAAAAACGG CTCGAG 1756

(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1286 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

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GCCTAGGATC CCTGTGACCC TCAACATGAA GATGGTGATG CCCTCCTGTC AAGGCCTTGA 60
TTGAGCATGA AATGAAGAAC GGGATCCCTG CCAATCGAAT CGTCCTGGGA GGCTTTTCAC 120
AGGGCGGGGC CCTGTCCCTC TACACGGCCC TCACCTGCCC CCACCCTCTG GCTGGCATCG 180
TGGCGTTGAG CTGCTGGCTG CCTCTGCACC GGGCCTTCCC CCAGGCAGCT AATGGCAGTG 240
CCAAGGACCT GGCCATACTC CAGTGCCATG GGGAGCTGGA CCCCATGGTG CCCGTACGGT 300
TTGGGGCCCT GACGGCTGAG AAGCTCCGGT CTGTTGTCAC ACCTGCCAGG GTCCAGTTCA 360
AGACATACCC GGGTGTCTATG CACAGCTCCT GTCCTCAGGA GATGGCAGCT GTGAAGGAAT 420
TTCTTGAGAA GCTGCTGCCT CCTGTCTAAC TAGTCGCTGG CCCCAGTGCA GTACCCCAGC 480
TCATGGGGGA CTCAGCAAGC AAGCGTGGCA CCATCTTGGA TCTGAGCCGG TCGAGCCCCT 540
GTCCCCACCC TTCCTGACCT GTCCTTTTCC CACAGGCCTC TGGGGGCAGG TGGCAAGGCC 600
TGGCCGGGGC TTCCTTCCTG GCCTTAGCCA CCTGGCTCTG TCTGCAGCAG GGGCAGGCTG 660
CTTTCTTATC CATTTCCTTG GAGGCGGGCC CCCCTGGCAG CAGTATTGGA GGGGCTACAG 720
GCAGCTGGAG AAAGGGGGCC AGCCGCTGAC CCACTCACTC AGGACCTCAC TCACTAGCCC 780
CGCTTTGGGC CCCCTCCTGT GACCTCAGGG TTTGGCCCAT GGGGCCCTCC CAGGCCCTG 840
CCCCAACTGA TTCTGCCCAG ATAATCGTGT CTCCTGCCTC CACTCAGCTG CTTCTCAGTC 900
ATGAATGTGG CCATGGCCCC GGGGTCCCCT TGCTGCTGTG GGCTCCCTGT CCCTGGGCAG 960
GAGTGCTGGT GAGGAGGTGG AGCCTTTTGA GGGGGGCCCT CCCTCAGCTG TTTCCCCACA1020
CTGGGGGGCT GGGCCCTGCC TCCCCGTTAC CCTCCTTCCC TGCAGGCCTG GAGCCTGTAG1080
GGCTGGACTG AGGTTTCAGT CTCCCCCAG CTGTCTCACC CCCACTTTGT CCCCCTCTA1140
GACCAGGGAG GCASTGGGGG AGGAGTTGTG TCTCGTCTTC TGTCTCCATG TGGTTTTTGG1200
GTGTTTTTCT TGTGTGTCC TGGATTCCGA TAAATTAAA GAAATTGCTT CCTCAAAAAA1260
AAAAAAAAA AAAAAAAGT CGACGC 1286

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(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

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ATTCGGCAAC GAGGTGAGAA AATCCCTTTT AAGGCCAAGG AAAGCTGAAT GCTAGCAGCC 60
AGGCCTGTGG TACTTCCATG AGAAACCATA GCAGACAATG CCCTCCCAAG TACTGAAATC 120
ACACTGGAAT CCCCTTGTT GGGTTCATTT GATTGTTTAA CACAGGATGT GTTGTGTCAT 180
TCTGAAGTTT TTATTTGGGG CAGAAGTCTT TATGGAGATG TAAATGACAG CGTTTCTGGG 240
TTATGCATAA CTTCTCACTG GTCAGAGACA CCGGTGTGTC AAGCATGGAT ATTGCATTGC 300
AAGACTTGAA TCTATAAAAA TTAGAATCAC ACAGTCAGTA CTACAAGCAA AACAGAGAAC 360
CTGAAAGAAG GTGCACAGAC TGTAAGAAAA AACCCAAGTT TGTGATATTT CAGTGATTCC 420
AAAGAACATT CTAGGTTTTT TGTGTGTTTT TTTGTTTTTT GGGTTTTTTT TTTTACTGCA 480
GAAAATTGGT GGTATTTTCA CATTCATAGT GTTTCTATCC AATTTCAGTA CCCACATTTA 540
ATGAGGAAAA AATGTTTAC CAATGAAGGA GGAATTCTTA AATTAGCTGT AATGTTAGGT 600
TGGAGAAAAT TTGGTATTTA GGGTATTTTC AAGGTACCAT CAAATCAGAT TTCTGTTTTT 660
TTGTTAAAAA AAATTTTTTT AATCAGTATT GTTTTTACAA GTAATATACT TTGAAACTCT 720
TGAACTAATA GTCTCAAAAA CTCTAGAGGA CAGTCTGAGA ACACGTATTT CTATTGTTCT 780
AAATAAATAC ATGTTTTTGA ATAGTTCAAT CATGAATTAT TGACTATGTC TTCATCAAAA 840
GTGTTAATCC CTCTCAGGGT CTCTGGTGAA GACCTTCAAG AGTTTGGTTT TTTCTCCCAG 900
GAAATTGGAA GGTAGAATTG TAAATTCATA GAACTTCTTT TATAATGGTG TACCTCAGCA 960
GCTGCCTTTC AATTATAGCC AAGTCCTTAC AGAGTTTATA CTTGAATAGT AAATATGTCT1020
TCTGAGTTTT ACAGTGTCTT AAACCAATG CACATTTTTT TTTCTTCTTT TTCCACCCCT1080
TCTTGTGTTG AGTTCATTAT ACCTGTCCTA TTACAGAACT GATTTCTTTC CTGGCTGTAC1140
ATGTTGGGGT GCTGGATTTT TTTCCGTGTC TTTAGTCTTC GGATACATGT TCTCTTCTTT1200
AGCTTGTGGT GAATACAGTA ATTTGCATTG 1230

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(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2328 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

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TGAGAGTTTA GTTGTAGCAG AGGGGCCACA GACAGAAGCT GTGGTGGTTT TTACTTTGTG 60
CAAAAAGGCA GTGAGTTTCG TGAAGCCTGG AAGTTGGCCA TGTGTCTTAA GAGTGGCTGG 120
ACTTTGACAT GTGGCTGTTT GAATAAGAGA AGGACAAAGG GAGGAGAAAG CACATGTGCT 180
CCAGTGAGTC TTCGTCACTC TGTCTGCCAA GCAATTGATA TATAACCGTG ATTGTGTCTC 240
TGCTTTTCTT CTGAAATGTA GATAACTGCT TTTTGACAAA GAGAGCCTTC CCTCTCCCC 300
ACCCCTGTGT TCTTGGGTAG GAATGGGAAA AGGGGCAACC TACAAAGATT GTTGGGGCAA 360
GGGAAGTCAC AAGCTTTCGG ATGGGCGGTG GCTTTTCACA AAACATTTAG CTCATCTTAT 420
TCTCTCTTGT TCCTCTCTCC CCTCCTGCCC GCCCGCACCC TGGAATTGCC ACTCAGTTCC 480
TCTGGGTGTG CACATATGTT TGGAGAAATA GAGGAGAGAA AAGAGGGCCA CGTAACTGAG 540
AGCTTACAGT GCCAATGCCG TTTGTGTTCT GGCCAGAGTG GAGTGCGCAG CCTGACTCCC 600
AGGCGCTGAG ATTGTTGCCT GGTTACCCAG GAAGCTGCTG TTCCGGCTGC CCAGCCTTTC 660
TCTGAGCCAG CGGATGCACA GTCCGTGGCC TTCTTCAGGC TTATTGATGA TGCTTTTTTC 720
AAATGTTGAA TCATGTTTCT GTTTCTAAGT TGGATCTTTT TTGTTTTCTC CTTGCCACCC 780
TAATTTGACA TCAAAATTCT CTCTTGTGCA TTGGGCCCTG GGTCAATCAA ACCCAGGTCA 840
CCTCATTTCC CTTCTCTGTT CACACCTAAT GTCTTGAAGA GTAGGTAGCA GCAGTGTGGG 900
CTGAACCTAG GCCAGCTTGC TTAGCGGGTC ACCCTGCTGT GAAGTCCTGG CAGGTGTTGG 960
TAATGTGTGG AAATGCAGTC AGCAAGTTTG CTGGGGAGTT TGATAAAAGT ATAAAACAAA1020
ACAAAAAAG CCTCGGTATA ATTTTGTTC ACGACTTCTT CTGTAGCTTT ACACCAGAAG1080
GAAGGAATGG GCTACAGCAG GTAGTGGAGG AAGAGGGGGG TGAGCAGGTG TATTAATAA1140
GCTTACGGGT AAGGCCTAAA AGGTCACCCC TCGGCCCCCT CTCCAAAAGA AGGGCATGGG1200
CACCCCCAGG AGAGGATGGC CCAAAAACC TTATTTTAT ACATGAGAGT AAATAAACAT1260
ATTTTTTTTA CAAAATAAC TTCTGAATTT ATCAGTGTTT TGCCGTAA AATATTCCTC1320
TATAGTAAAT TATTTATTGG AAGATGACTT TTTTAAAGCT GCCGTTTGCC TTGGCTTGGT1380
TTCATACACT GATTTATTTT TCTATGCCAG GCAGTAGAGT CTCTCTGCCT CTGAGGAGCA1440
GGCTACCCGC ATCCCACTCA GCCCTCCCT ACCCCTCAAG ATTTGATGAA AATTCCAACC1500
ATGAGGATGG GTGCATCGGG GAAGGGTGAG AAGGAGAGCC TGCCTGCTCA GGGATCCAGG1560
CTCGTAGAGT CACTCCCTGC CCGTCTCCCA GAGATGCTTC ACCAGCACCT GCCTCTGAGA1620
CCTCGCTCTC TGTTCCAGCA ACCCTGGTTG GGGGGTCAGA CTTGATACAC TTTCAGGTTG1680
GGAGTGGACC CACCCAGGG CCTGCTGAGG ACAGAGCAGC CAGGCCGTCC TGGCTCACTT1740
TGCAGTTGGC ACTGGGTTGG GGAGGAAGAG AGCTGATGAG TGTGGCTTCC CTGAGCTGGG1800
GTTTCCCTGC TTGTCCAGTT GTGAGCTGTC CTCGGTGTTA CCGAGGCTGT GCCTAGAGAG1860
TGGAGATTTT TGATGAAAGG TGTGCTCGCT CTCTGCGTTC TATCTTCTCT CTCCTCCTTG1920
TTCCTGCAA CCACAAGATA AAGGTAGTGG TGTGTCTCGA CCCCATCAGC CTCTCACCCA1980

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CTCCAGACA CACACAAGTC CTCAAAAGTT TCAGCTCCGT GTGTGAGATG TGCAGGTTTT2040
TTCTAGGGGG TAGGGGGAGA CTAATTCGA ATATACTTA AAATGAAAGT ATACTTTTTA2100
TAATTTTCT TTTTAAACT TGGTGAAATT ATTTAGATA CATATTTTAG TGTCAAGGCA2160
GATTAGTTAT TTAGCCACCA AAAAAAGTA TTGTGTACAA TTTGGGGCCT CAAATTTGAC2220
TCTGCCTCAA AAAAAAGAAA TATATCCTAT GCAGAGTTAC AGTCACAAAG TTGTGTATTT2280
TATGTTACAA TAAAGCCTTC CTCTGAAGGG AAAAAAAAAA AAAAAAAA 2328

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(2) INFORMATION ON SEQ ID NO. 237:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1767 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

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TGTGACATTG TCCTGAGGTT CATCCGCCTA AATTATTATT AGCCATCCCT TACCAAATAT 60
TTCAAACCAG GCAAATGACT TCTGGAAGAG AGAGAAAGGA AGGGGAGAGG GAGGGAGAAT 120
ATGAGTAAGC AAGCAGGGTC ATATGGTTAA ACATGGAATT TTTTAAAGGA GTTATTACAA 180
GTGGGAGTCA AATAGAACTG TGGTAGAATG CTTTGGGTAC AGGAATATGT TATGCAATAA 240
AGTGAGGAAG AGAAAAAGGG AATAAGAAGG GAGGAATGTA ACTAGAGCAG CTCCCAACAG 300
TTTGCCCTATG TATTTGCCAG CACCAAAATT CGTAGAGTAA GCCACTTACA TTTCCACTGC 360
TAGTATTAAG GAAAGACAGC AGTGGTGATT CTTATAAAGT GAGTATACAT TTATTCTTAT 420
TCTGATATGT GAATTTTCTT TTCACCACTT AATTAAGCTG TAATTTGTAA ACAGTGGGAA 480
GAAGATTAGA ACAATTATGG AGGTACTGAA TTACACAAGG AGATTAAAAT GAAATGAATC 540
AAACTAACCA CAAGATAGGT AGATTGATTC ATTTTCATTT AATCTCCTTG TGTAATTCAG 600
TACCTCCATA ATTGTTCTAA TCTTCTTCCC ACTGTTTACA AATTACCAGT TAATTAACCTC 660
GTGAAAGAAA AATTCACATA TCAGAATAAA AATAAATGTA TACTCACTTT ATAAAAATCA 720
CCACTGCTGT CTTTCTTAA TACTAGCAGT GGAAATGTAA GTGGCTTACT CTACAAATTT 780
TGGTGCTGGC AAATACATAG GCAAACCTGTT GGGAGCTGCT CTAGTTACAT TCCTCCCTTC 840
TTATTCCCTT TTTCTCTTCC TCACTTTATT GCATAACATA TTCCTGTACC CAAAGCATTC 900
TACCACAGTT CTATTTGACT CCCACTTGTA ATAACCTCCTT TAAAAAATTC CATGTTTAAAC 960
CATATGACCC TGCTTGCTTA CTCATATTCT CCCTCCCTCT CCCCTTCCTT TCTCTCTCTT1020
CCAGAAGTCA TTTGCCTGGT TTGAAATATT TTGTAGGGAT TGCTTATTAT ATTATTTTAG1080
CTGATGAACC TCAGGACAAC GTCTACACAC ACACACATAC ATACACGCAC ACAAATCTC1140
AGCTGTTGAA GAGTGGGCTT GGAATCAGAC TTCTGTGTCC AGTAAAAAAC TCCTGCACTG1200
AAGTCATTGT GACTTGAGTA GTTACAGACT GATTCCAGTG AACTTGATCT AATTTCTTTT1260

GATCTAATGA ATGTGTCTGC TTACCTTGTT TCCTTTTAAAT TGATAAGCTC CAAGTAGTTG1320
CTAATTTTTT GACAACCTTA AATGAGTTTC ATTCACTTCT TTTACTTAAT GTTTTAAAGTA1380
TAGTACCAAT AATTTTATTA ACCTGTTCTC AAGTGGTTTA GCTACCATTC TGCCATTTTT1440
AATTTTTATT TAATTTTATT TGCTTGAGCA CACTGATCAA CCACTGAACT GCCTTCTTCC1500
ATTGTCCTGC AATGATATAA GGGTTACATT TTTGTGTATA TGGCTTTTCAT AGTTGGGATT1560
TCAGAGCACT GATACCAGAT ATTTTCAGTT TGTTCTCTGG GGAATTTTCA TTTGCATCTA1620
TGTTTTTAGC TATCTGTGAT AACTTGTTAA ATATTAAAAA GATATTTTGC TTCTATTGGA1680
ACATTTGTAT ACTCGCAACT ATATTTCTGT AAACAGCTGC AGTCAAAAAT AAAACACTGA1740
AAGTTTTTCA TTTGCAGTGG AAAAAAA
1767

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(2) INFORMATION ON SEQ ID NO. 238:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2311 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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CATCGCCTTC ACCGGCGGCG GCAACATCGT GGTGGCCACG GCGGACGGCA GCAGCGCGTC 60
GCCCCGTGCAG TTCTACAAGG TGTGCGTGAC GTGAGTGAGC GAGAAGTGCC GTATCGACAC 120
GGAGATCCTG CCCTCCCTGT TCATGCGCTG CACCACCGAC CTCAACCGCA AGGACAAGTT 180
CCCCGCCATC ACCCACCTCA AGTTCCTGGC CCGGGACATG TCGGAGCAGG TGCTTTTGTG 240
CGCGTCCAGC CAGACCAGCA GCATCGTGGA GTGCTGGTCC GTGCGCAAGG AGGGACTCCC 300
CGTGAACAAC ATCTTCCAGC AGATCTCCCC CGTGGTTGGC GACAAACAGC CCACAATTCT 360
CAAATGGCGG ATCCTATCGG CCACCAACGA TCTGGACCGT GTGTCGGCCG TGGCGCTGCC 420
CAAGCTGCCC ATCTCGCTCA CCAACACCGA CCTCAAGGTG GCCAGCGACA CACAGTTCTA 480
CCCTGGCCTC GGGCTGGCCC TGGCCTTCCA CGACGGCAGC GTCCACATCG TGCACCGGCT 540
CTCACTGCAG ACCATGGCCG TCTTCTACAG CTCCGCGGCC CCGAGGCCTG TGGATGAGCC 600
GGCCATGAAG CGCCCCCGCA CCGCGGGGCC CGCCGTCCAC TTAAAGGCTA TGCAGCTATC 660
GTGGACGTCA CTGGCCCTGG TGGGGATTGA CAGCCACGGG AAGCTGAGCG TGCTCCGCCT 720
CTCACCTTCC ATGGGCCACC CGCTGGAGGT GGGGCTGGCG CTGCGGCACC TGCTCTTCTT 780
GCTGGAGTAC TGCATGGTGA CCGGCTACGA CTGGTGGGAC ATCCTGCTGC ACGTGCAGCC 840
CAGTATGGTA CAGAGCCTGG TGGAGAAGCT GCACGAGGAG TACACGCGCC AGACCGCTGC 900
CCTGCAGCAG GTCCTCTCCA CCCGGATCCT GGCCATGAAG GCCTCGCTCT GCAAGCTGTC 960
GCCCTGCACG GTGACCCGCG TGTGCGACTA CCACACCAAG CTCTTCCTCA TCGCCATCAG 1020
CTCCACCCTG AAGTCGCTGC TGCGCCCCCA CTTTCTCAAC ACGCCTGACA AGAGCCCCGG 1080

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CGACCGGCTG ACCGAGATCT GCACCAAGAT CACCGACGTC GACATTGACA AGGTCATGAT 1140
CAACCTCAAG ACGGAGGAAT TTGTGCTGGA CATGAACACA CTGCAGGCGC TGCAGCAGCT 1200
CTTGCACTGG GTGGGCGACT TCGTGCTGTA CCTGCTGGCC AGCCTACCCA ACCAGGGTTC 1260
CCTGCTGAGG CCGGGCCACA GCTTTCTGCG GGACGGCACC TCGCTGGGCA TGCTTCGGGA 1320
ATTGATGGTG GTCATCCGCA TCTGGGGCCT TCTGAAGCCC AGCTGCCTGC CCGTGTATAC 1380
GGCCACCTCG GATACCCAGG ACAGCATGTC CCTGCTCTTC CGCCTGCTCA CCAAGCTCTG 1440
GATCTGCTGT CGCGATGAGG GCCCAGCGAG CGAGCCGGAC GAGGCGCTGG TGGATGAATG 1500
CTGCCTGCTG CCCAGCCAGC TGCTTATCCC CAGCCTGGAC TGGCTGCCAG CCAGCGACGG 1560
CCTGGTTAGC CGCCTGCAGC CCAAGCAGCC CCTTCGTCTG CAGTTTGGCC GGGCGCCCAC 1620
GCTGCCTGGC AGTGTGCCA CCCTGCAGCT CGACGGCCTC GCCAGGGCCC CAGGCCAGCC 1680
CAAGATCGAC CACCTGCGGA GGCTGCACCT TGGCGCTTGC CCCACGGAGG AATGCAAGGC 1740
CTGCACCAGG TGCGGCTGTG TCACCATGCT CAAGTCGCCC AACAGAACCA CGGCGGTGAA 1800

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GCAGTGGGAG CAGCGCTGGA TCAAGAACTG CCTGTGCGGT GGGCTCTGGT GCGGGGTGCC1860
CCTCAGCTAC CCCTGAGCCC AGCTGCCCCCT CAGCTACTCC TCAGCTACCC CTCAGCTGCC1920
CCTGAGCCCG GCTGCTGCAA GAGCCACCGC TCGCCCTGGA CTCTCCTCGG CGCGGTTAAC1980
CTCAGCCCCG CCTGCAGGGC TGTTGAAGGC CGTGGGCCGG ACGCCTGCGT GACCAGCAGA2040
GCTTCTGAGG AAGCCCCCTGC CTTTGTCCAG CTGGGCCCCG AGTCCACACA CCACTCTCCC2100
AGGACCCCCA GATCCCTGGA CCATCTGCAT CCAGAGGACC GTCCGTGACG GCCGGGGGTC2160
CAGGCGGACC TTGTGGTGAC CCGGCTCGGG CGTCTCCTCG GTTTCCTTGC CTCACCCGCG2220
GAGAGCGCTG AACCTGGACA AGCAGCGGCT GGGAAGGACA GGTCCAATAA ACGCCCTCTG2280
CGCCAAGAA AAAAAAAAAA AAAAAAAGGG G

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2311

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1772 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TGGGCGCTGT AGTCCGGCCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60
 CTCACACCCC AGTCCGCAGT GCCCCTCCCC AGCCTCGGCC GGGCCTCCCG GGAGCCGGGC 120
 GTGGCGTTCC AGCTAGTGAG CCGTTTCTCC CCTGGGCTCG GAGGCGGAAG CTTGAGGGGC 180
 GCGGGGAGGA GCTTCGCGTG CGGGGTGAAC GCCCGCTCTA CGTGCTCGTT CTCTTCGCGA 240
 CCGCTGCGCG CGAGCCCCGT GTCCCCACGG CGGGCAGCAG CGCCGGCGGC GGCGGCTGAA 300
 CGCGGAGGGG GCGGAGGGAG CCCGCGGCGG CGGCAGCAGC TACAGCGAAA TGGCGGAGAC 360

CGTGGCTGAC ACCCGGCGGC TGATCACCAA GCCGCAGAAC CTGAATGACG CCTACGGACC 420
 CCCCAGCAAC TTCCTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCCGGGG 480
 CCGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540
 ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600
 GAGCAAGGTC GTAGTTCCCC CGCTCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660
 GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720
 TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAACG AACGTTGTCT TCACATGTTT 780
 TTACAAGATG AAATAATAGA TAAAAGCTAT ACTCCATCTA AAATAAGACA TGCCTGAAAT 840
 TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTTC 900
 TAACTTTTAG CATGCTGCAC AGAAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960
 ATGCTCAGTT TTGTTTTGTT TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020
 CCTCATTTCA GCCTTTCTAT ATAAATAGCT CTTTCTTGCT GTTTTAATGT GGTGCACACT1080
 ATAGCCTCAC AAACCTGTTA TTCCAGTGTA ATCTGCAGTG TCGTAACTAA AGTTACTGGC1140
 TTGGTCTTAT TTGCACAGTT TTTGCGTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAAT1200
 ATTTCTCTTT CCCCCTTTTA ATTTGTGATG TCACTTGACC CCATTTATGT GTAGGAGCAC1260
 TACACCATTG GTTTCCAATA CTGCACACAT AAGATACATA CTTGTGTGCA GAAAGTATCT1320
 TCCTCCAGGC TTGTAATACC CTTACATGG AAGATTAATG AGGGAAATCT TTATATTCTG1380
 TATAAAAACA AAAGCAAATT TATATACTAA AATCATTTGT CTAAAAATTT AAGTTGTTTT1440
 CAAATAAAAA TTAAATGCA TTTCTGATAT GCACTGATTG TGTTGCCTCC AGCTTTTTTT1500
 GCTCTCTATG AGTGACTACT TAAGTCACTT GTTGAGAGGG ATTATTTACT AATTATATAC1560
 TTCTCATTTCC TGTAACCTCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620
 ATTGAATGGG GTATTTTAA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTTAAG1680
 GCTTATTGAA TCATTTTGAA GCACTTTGTG TATTTGAAAA CTGCTTTATA ATCTCATTTA1740
 TTAAAAGGAC TTTCAAAGAT AAAACCAAAA AA 1772

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

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TCTGTATCTT CTTGCCCCTC AAATACCCTG AGGTGATAAA CTGTTCCAGT TGTAGCCAAC 60
TACCACTGCG CCCGGCCTTA AATAAAATAT TGTAGTCATT AATGGTGTGT TTGAATTGAA 120
GAGATACCAG GAGATAGAGG TGAAGTGCAG TACTTTTATT CTTTAAGAAT ATAGTCTTTA 180

GCCAGGTGCA GTGGTGTGTG CCTGTAGTCT CAGCTATTTG AGAGGCTGAG GTGAGAGGAT 240
CACTTGAGTT CAGGAGTTCA AGACCAGCCT GGGCAACATA GCAAGTCCCT GGCTCAAAAA 300
AAAAAAGTT TCCCATTCAAT ATTAACCTCA TCTTTTAAAA ATGTCATGAT TACAAAGTGA 360
AAAGATTTGG CTTTCTTAGA GGCTCAATCA CAGAGGTGAA AGTGACCTTG GAAATCATAT 420
ACTCTATCCC CATGTTACAC AGATTAGAAA AACTGAGGTT ATGGCACTGA CTTAGGCACC 480
CCCCAGCAAG GCAACCCAGG GACTACAAC TGGCAATCCCA ACTCCTGGGC TAGGGCTTTG 540
TCTACCTTTT TTTGCATTGG CCTCTTAAAG AGGCAATGAA TACTAATTCC TGGCATCAGA 600
AAAAAAAAAA GGCATGAGGT GGGAGGATTC TTTTTCCTCT GATGGGAAAC AGTGAATAAG 660
AAAAATCTCA TCATTTCGATG GAAGAGGTGA CTTAATAATT TTATTAATGA ATTTGATGTC 720
CCATGTTTTG TAGTTTTGTT ATCATTGAAC CATTGGGGCT GGAATCTGCC TAAATAATTT 780
TATCTTGGA GCCAGCAATT ATGTTGGTAT TTTATGTGGG CCTTCCCAGA TTTTCATATT 840
AATGAAATGA CTAATAGTCG TACTTAAGAG GTAACCTCTAC TAAAGCAGAA TGAGATCTAA 900
TATGTTGTGG AAATAAAAGA GTTTGCAGTG GAATGATACT CTCACTCCGT GCTTGTAATA 960
TTGAGTTCTA TTCAAGACGG AACTGCTATG ACTGGCCTAT TCAAGGCTTC ATATTTTAT 1020
ACAGACTATT TCACAGACCA TAGATTTATT TTAAGAGGGA AAATCTCACA CATAATTAAG 1080
CAGTGGAAAA TGTGCTCAAT GCTATGGTGT GTCAGGCCCT CTGTCTACCA GGTTCCTCCC 1140
GCTTCTGCA GAGCTGTGGA CCCTGTACGT ACCAAACAGG TGAACCTGGT CCATCTTCC 1200
TTCTTCCTTT TTTTGCACAT TTGCATTAT ATCTTCCTGT ACTAAAAGAA ACAAAATTAT 1260
TATAATTGGG GTGACAATAT AAAGGAACAA AAGATGGGGC AATACTTGCT TCCTAGCTGG 1320
AGCTGTAAGT CCATGTTACA GAACTCACT ATTTAAAAAG TTTTAAAAGA TTTATGAACC 1380
TTGTCTTACA ATTCGCTGAA TACTTATTTG TCTTTTAAAC TCCCCTCGGT GTATGGATCA 1440
TCTTCGTCAG AATGCCGTTG TTTTATTGTG AATCAGGGGA AAATGTTAAT CATTTGGAGA 1500
CTGTTTTCTT ATTACCAAAT GTACAATCCA TAAGACAAC TAAAGCAACA ACTGCTGGGT 1560
TCACTGACAA AGATTATAAA AATCATCACG TTCAAAGTAG AGTTTTTAGC CAAGGTCAAG 1620
AACTAACCTG GGGCTGAGTC AGCGTCTCTA CCCACTTAAA TAACAGCGTA AAGATCTTTC 1680
ACTAAATTCG TTATGTGGTC TGTCTGGATG TAAACCTATA TATTTCTTTT TGAAACAGAA 1740
TCATATCCTG CAGACTCTTG GCACTCCTGC ATAGCTTTGA CCGAATGTTC ACTCTCATCG 1800
TAATGGAAGA TTTCTATCTA TGCAGATAAT ACATGTTTTT AAATACTGTT TTCTGTTTAG 1860
TCCTCAATCT TCCTAACTCA AATTGGGGAC TGAGGAGAGA GAAAGGTGGT TACCCCTGTT 1920
ACCGTGCCAT ATTCTTCTTG CTGCTTTTCA ACCCCACGTG ATTGTTGATT GACGGTTCTG 1980
CTATAATGTG CGTGCCCTTC AAGTTTCAGA AAACCTTCCC AATCATTTCA CTTCAATCTT 2040
AATTGAACCC AAGAGTCAAA GTTATTATTT TCTCCGAACG TGTTTGTGAT CTTCTGTTAT 2100
ATTTTGGGGC ATGTTACCTT TATGGTATAT AAGCTGTAGT GCATACTCTT TGTATTGCAA 2160
AAAACCTGGT AGTAATTTAT GTACATGTAT TCCACATTTT AGTGTGCTTG AAGTGACAAT 2220
CCATAGTTTG TAGTAGTTTG TTATTTGTCA ACTTTACCCT GTGTTTTAAG GACATCTAAA 2280
CATTCCTTGT CCTATCAAGA TGACAAAAGC AGAATGTAAT TTTTTTTTGG AAGCTTCGTG 2340
ATTACCTGTA ACAAGTTCTG TTTTAAAAAC GAATACAAAT AAAGTTAGTA ACTATTTTTA 2400
AATCAAAAA
2409

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(2) INFORMATION ON SEQ ID NO. 241:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2594 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CGCCCTTTTT TTCTTTATTT TCTTATGTAC TCATCTACTT ATTCTCAAAG TATTTAGCAT 60
TCAACACTCT TTTTGCTTTA AAAAGAATGG CCTTACAAAG GGACAGAAAA GAGAAGACAC 120
GAGCTTGGTG TATTTTCATC AAGTTATGTG GCAGAGAAAT CCAGATATTA CCAGGACCTG 180
TCTAAACAAA TGTTGTGGGT TTTCTTTTCA TTCGGATAGC CACTTTATAG TTGGAATATC 240
AATTCTAATG AGGAGGAAGA CATAAATATA AGTGGTAAAA AGAAACATGA CTTCCTTAA 300
AACAGGCTGG ATAATCTATA TCAGCCTTGT GGGTGGAGAC TAGTATTTGA TCCTTGCCAT 360
ATAAAACATT TTAATATGGT TTACATGGGA AAATATCGAT GGCTTCCTCA CAAAATGTAT 420
GGGTGACGTG AAGTTGAAGA GCCAATGGCT TGGGTGACAC GTGCTGGATC CAAAAGATC 480
AGGGAGACTA GAATAAACT TGGATGTTAA AAATTCACCA GGAATCCACA TAAAGTACTA 540
TATTTGGGCT AAAATGAAAA ACTAAATACA AGGTGGGAGA GAGGCAAGAA TTTCAGTTGA 600
CTAAGCTCAG TGTGAGTTCA AAGTGGGATG GAACCATGCA AAAACAAAAC CCACAGACAT 660
GCAGGCTACG TGAGGAGAAA ACAGTGGTGA GGATCACATC ACATTGTGTT TGCATTTGCC 720
GGAACCATAC TTTAAGAAGA AAACCGATCA TCTATAATAA CATCAGTTTA TCAATGCCCC 780
GTCCTGATGA AGTGTGCAGA CTCTCAGAAA CAGCAGGAAG GACTTCATGA GAACCTCAG 840
GCTGGAGAAG GGACTAGGGC ACAAGGAGAG CTCTCCTAGG ACCAGGACCA AGAAGCTACA 900
GGCAGGCACA GTTTAGCTCC TGCAGAGACC CAGCTTTTCA CAAGTTGGAG CCTTCCAGAG 960
ATAGAGGGAC TGTGGTAGGT GGTGACCCAC CCATCACTGG AGGTGGAAGC AGAGGCCGTT1020
TGCCAGGGAT GCTGGAGAGG GGATTCAAGC ATCTGGCTGG GCAACGTGAT GCTCAGGGCC1080
GTCTCCACTC AGGGCTTAGG GGAGTCTGTG AGTAGAAGAG CTTTAGGTGA TTTGTTTGGT1140
GGGGGAAGGC AAGTACACAG CTATGCACTT TCCGTTTCTG ACTTTTGCCA CCCTGTCAGC1200
CATGGGGAGC CCACTGTGGG ACTGAAACCC TGAGCTGAAT GCGGCCTCAT TCTCAGAGA1260
AACACTGGCA AGTTGGTCAG AGCCGCCGTC TGCATCGAGG CGTACTGAGC GGCAGGATGG1320
GGGGCTGCCT GCCCAGGGTC TCTCACCGTG GTGTAAGCAG AGCCATGGCT TGCCTAGGAC1380
CCTATAGATA CCATCACTCT TTCTCAGCTC GACTGGAGTT TCTGCACCTT TGCAGGGGCA1440
AAGTAACTCC CTGCACCTG AACCACCCCT CATTCTGTG CATTTCAGCA GATAATGATG1500
GAGGGGGGGG GGTGTCCATC GTGCTGAGGG TGTGACCGCA AGAGGGTGAA AACTTCCAGC1560
CAACTTTCTC AGTCCTTTCT CTTGCGAGAG GGAAGCCACC TGCTATACAA ACTAATACCC1620
CCTGCCTTGA CCCCTTCCCC ACGACTCAGT TGACAGAAGG ATATACTTTG TTATAACTTA1680
TTATTTTGT CTCTGTAAAT ACAAGATGTT TATAGGAAAT ATGTATTCTG AACTCTATCT1740
GCAGAATGAG TCACTACACC AAAATAGTTC TATTATTTAG AATGTGTTAA TTTTAAAGGG1800
ACCTGATAGG TATTTATTTA CATATGCGAT CCACATTTGT GTGAAAGCAT GTGATCATAC1860
TAACCCAGCC TCCTGGAATG TCGCTGTACG ATGATTGATG TCTTTTTCTC AGTCCATAGT1920
TACAATTGTT TAGTATGCTA ATCAGTCCAG TTCCCTGAGG TTTAAGATCA AATATAAATT1980
ACTCTGCTTT TCGACTCATT CAGGTAGCAT TGTACCTGAA CCTGATTGCT ACTTTTTCAT2040
CTTAAATATT ATATTTCTCT ATCTAATCTG CCTCCCCCTC ATCCACAGAC ATTTGGAGAA2100
GGAAATGGGA GGGTGTCTGT TATCCCTTTC TCTTTGCTTT GTCCCCGTTG TTAGACTGGC2160
AGCGTCAGTT GCTCGGTGGG CTTGGTTAGA GCCGTGGGTG AGGCAGGTGG CTGGCGGGGA2220
CAGGGAGAGG CTGAGAGGGA AGTGGTGGCA TTTACTGCTC TGACACTTCC ACTGTCCCTG2280
CTGGGGATGC TGGGGCCAAG GCCTGTGGGG CCTGTGAAC GCACAGCCAG GAGCAAGGAA2340
CCCATAAAT ACTCCGTCAC CTCCATGTCC CCTCTACAG GTTAAATTAT TACATAAGCA2400
GGTGAAAGGT AGAAGGCGAA TTATGTGAGT AAATATGGTC TGTTTTCTCT TCAGCAAAAA2460
TGACTATTTT TGTGTGTGAC TAATTTATTT TTATTATTGT AAAGATACAA TAAACCGGTT2520
GAAATATCTG CTTTGTGAC AAGCGTGTGC TTTCTATGGC NTTATTNGCG TTCTGTTNTC2580
CTGNAAATAG CGCC 2594

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1012 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

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TGAAGTGGAG AGGTGAAGGT TGCAGTGGCC TGAGATCGCG AAACAGAGCG AGACTCCATC 60
TCAAAAAATA AATAAATAAT AAAATTGGCC GTTACCGGTG GCTTATGCCT GTAATCCCAG 120
CACTTTGGGT GGCCGAGGCG GGTGGATCAC CTGAGGTCAG GAATTCGAGA CCAGCCTGAC 180
CAACATGGAG AAAACCCCGT CTCTACTCAA AATACAAAT TAACCGGGCG TGGTGGCGCA 240
TGCCTGTAGT CCCAGCTACT TGGGAGGCTG AGGCAGGAGA ATCACTTGAA CTCAGGAGGC 300
AGAGGTTGCA GTGAGCTGAG ATCATGCCAT TGCACTCCAG CCTGGGCAAC AAGAGTGAAA 360
CTCCGTCTCA AAAAAAAAAA AAAAGAGATG TTTTTCATTT TTTTCATGTT ATCTATCCAA 420
GCACTGTTCC ATGGTCAGCA AGTCATATTT CATAATGTGG ATTTTCCAAA ATAATTATTG 480
AATACAGCTA TTCTATGGCT ACTTTTAGTG TTTTGTGGT ATGTGGTGTG GGAGTGTTTA 540
TGGAATTACC AGTATCTTAA ATTTTCAAAG GAACCTTGGG AGTCTATCAC TCTAAATGAA 600
AGTCTGTCAC TCTACATGAA TTATGTGCTC AAATTTGACC AACTCAGTTT AAGACACAAA 660
ACAGTAATTT GAAGAAGGAA AAATGAAGAG AGTTTCTAGT TTAATGGGTT AAATTTTGTG 720
TGTTGCAATA GTAAGTTTAG TCTTCTTATA ATATTTCTAA ATGAAAAATC ATAGGTATTT 780
GTTACCATGT GTGAAGATTA CTTTGTTAAA AGCAAAGTG GTCGTGTGAT ATGCTAAATG 840
TTAATTACTG ATTTTATATG TTAAATCAC GCCAAACAAA TTATGTCTGT GCCATCCAGG 900
GTCTGTTGTT AATCTTTTTC TGAGTACTTG GATTGGGATA AAGGGCTTGT ACTATGCACT 960
TTTTATTAAT GAATAAATAG AAAACGTTAG TAACAAAAAA AAAAAAAAAA AA 1012

```

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TGAGACGGAG	TCTCGCATCT	GTGCCCCAGG	CTGGAGTGCA	GTGGCGGGAT	CTCGGCTCAC	60
TGCAAGCTCC	GCCTCCCGGG	TTCACGCCAT	TCTCCTGCCT	CAGCCTCCCA	AGTAGCTGGG	120
ACCACAAGCA	CCCGCCACTA	CGCCCGGCTA	ATTTTTTGTA	TTTCTAGTAG	AGACGGGGTT	180
TCACCGTTTT	AGCCGGGATG	GTCTCGATCT	CCTGACCTCG	TGATCCGCCC	GCCTCGGCCT	240
CCCAAAGTGC	TGGGATTACA	GGCGTGAGAC	CGCGCCCCAC	ACTATGAGTG	TTTTTAACAC	300
CATTCTCCCC	CACTTCTCTC	CTGGGTGACA	TAAGAGAGAA	ATAACCNTGT	AGTACAGCAG	360
CTAAAGTATT	CTCCTTTCAG	AGAANNTTTT	TTTGGAGGTC	TCTAATATAT	ATTTCCCCCN	420
TTGTCTCTGT	GATCTCTTAT	TTATACTATA	TTATTGTCCC	ATGTACTTTC	TAAACTGAGC	480
TTGGAACATT	TAGTATTCCT	GCAATTGGAC	TTCCCACTTA	ACAATTATAC	AGACTTTGCT	540
TTTAGAAATA	GATTAGGTTC	CAAACAGAAA	GTTTNAANGT	GTAACAACNA	ACAATAAAAA	600
TAGATTATGA	AACANGGCTA	TAATTGGCTC	TTTTGGATTT	NGATAGGGGC	AAGATGAAAG	660
GNCAACNTTT	CTTGCNTTTT	GAAANNTCAT	NGTTNGGGTA	ANGAGGTAAG	GNAATNCCAG	720
CTANCAATTT	TNATTAGTGC	TTGNAAANCG	GGCTTNCCTT	NGAATTCNTC	CANGGNCCCT	780
ATCATTTTTT	TTTTCTTNAC	TAATNCAGAA	GAGAGNCTGG	GGTAGAAGNC	CCCATNGTTT	840
GTATTCCNAT	GAAACACNGT	CGGGTTGGNA	GTAAAGGCAA	AAACAGCNTA	GACACACCAG	900
GNTGTGTCTG	NNTTTGACAT	TTATAAGCTG	GCACTCATCA	ACACTCCTGT	TTCTCCTTTC	960
TCTGGGACGT	GTGGATTAAG	GGGTGTGAGT	TGTGGGAAGA	ATTGNCCCTC	GTACCTCCTG	1020
GATTTATTAT	TTTTCTCAAA	TACCAACCNA	GTAAGATCCC	AAATAACTTG	AGAAAAATTG	1080
TTTCCTGATC	TGTCCACTTC	TGGTGTCAAA	GATTTTACTC	ATCTTCTTAG	TACATTCTAT	1140
GTATTTTATA	TGTATAATTT	TNATACAATT	AAAAATAGAT	TTTTGTNCTA	GTNGAAAAAA	1200
AAAACA						1206

(2) INFORMATION ON SEQ ID NO. 244:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2514 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

U.S. GOVERNMENT PRINTING OFFICE: 1989-0-251-400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

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AAGGTGAAGA GCGGCATCCG GCAGATCCGG CTCTTCAGTC AGGATGAGTG CTCCAAGATC 60
GAGGCCCGCA TCGATGAGGT GGTGTCCCGC GCCGAGAAGG GCCTGTACAA CGAGCACACG 120
GTGGACCGGG CCCCCCTGCG CAACAAGTAC TTCTTCGGCG AGGGCTACAC GTACGGGGCC 180
CAGCTGCAGA AGCGCGGGCC GGGCCAGGAG CGCCTCTTAC CCGCCGGGCG ACGTCGACGA 240
GATCCCGGAC TGGGTGCATC AGCTGGTGAT CCAGAAGCTG GTGGAGCACC GCGTCATCCC 300
CGAGGGCTTC GTCAACAGCG CGGTCATCAA CGACTACCAG CCGGCTCCT GCATCGTGTC 360
CCACGTGGAC CCCATCCACA TCTTCGAGCG CCCCATCGTG TCGGCTCCT TCTTTAGCGA 420
CTCTGCGCTG TGCTTCGGCT GCAAGTTCCA GTTCAAGCCT ATTCGGGCT CGGAACCACT 480
GCTTTCCCTG CCGGTGCGCA GGGGAAGCGT GACTGTGCTC AGTGGATATG CTGCTGATGA 540
AATCACTCAC TGCATACGGC CTCAGGACAT CAAGGAGCGC CGAGCAGTCA TCATCCTCAG 600
GAAGACAAGA TTAGATGCAC CCCGTTGGA AACAAAGTCC CTGAGCAGCT CCGTGTTACC 660
ACCCAGCTAT GCTTCAGATC GCCTGTCAGG AAACAACAGG GACCCTGCTC TGAAACCCAA 720
GCGGTCCCAC CGCAAGGCAG ACCCTGATGC TGCCACAGG CCACGGATCC TGGAGATGGA 780
CAAGGAAGAG AACC GGCGCT CGGTGCTGCT GCCCACACAC CGGCGGAGGG GTAGCTTCAG 840
CTCTGAGAAC TACTGGCGCA AGTCATACGA GTCCTCAGAG GACTGCTCTG AGGCAGCAGG 900
CAGCCCTGCC CGAAAGGTGA AGATGCGGCG GCACTGAGTC TACCCGCCGC CCTCCTGGGA 960
ACTCTGGCTC ATCCTTACGT AGTTGCCCTT CCTTTTGTTC TGAGGGTTTT GTTTTTGTTC 1020
ATTGGGGGGT TTTTGTTCCT TGTTTTTTGT TTTTTTTGAT TCTATATATT TTCCTTGGT 1080
TTTGTGCTCT GTTAAGGCTG AAGAATAGAA TTGGCCAGGA CCTAGGTTCT CATATTCTTG 1140
GTATTCTCTC TGGATGGAAA GGCTGTTGGC ATCAATAGGG GACAGAGGCT GATGCTGGAG 1200
TGGCCAGTAG AGGTGGTGGA GCAGAGCAGC CATCTTTTAA GTGGGGCTGT ATCAGGCTGG 1260
GTTTATTTAA AAGCAACAAA ATGTTTTGGT TAAGAAAATT ATTTTGCTTT CAGTGTAAT 1320
CTTCGCAGTG TTCTAAACAA AGTTCAGTCT TCTGCTCGCC CCTTTCCCTC ACTGATGTCT 1380
GCACTTGGTT GAGGTCTCCT GGAGCCTCAC AGGCTCTGCT GTTCTCCACT TCTCACCTGC 1440
CATCCACGCC CTGCAAGCTC ATGCAACAC CCTTCTTCC TCCTGCGGCA GAGTTGTTCA 1500
GGTTGCCTGG GCAGGGGCTT AAACAGTGCC AGCCCTGCC ATCCCAAAGC TATTGTTAAG 1560
CCCCCAGGC GTCCTCCACC CACGCCCACT AGCCTGCCAT GTCCACAGTT CCTTGGGCTG 1620
CTGAGGGGCT AGTGCAGTGG TCCTGACCTC TCTTATCAAG AGCACACTTC TTTGCTGGTT 1680
GCTCCTTTTG AGCATATGCG TGTGATTATT TGGAACAGTT AGACTTGCCA CGTTGGGTCA 1740
GTTTTAGAAA TTGTTTCTAG CTAGAGGGAC TGGTGTCTT CCAAGTCTAG CATTTGGGGT 1800
ATGGAAAATT GTTGTGGTGT GTGGTAGGGT TTTTGTTCCT TTTTGTGAGT TTTTTTCCC 1860
CCTTTAGTCT CCTGGCTTTT TCCTTTCCCT TCCCTTCTCC ACTGGCCAGC TTGGGCCTCA 1920
TCCTCATGTC ATCCTTCTAG GAAGCGCCTT GCCCCATCTT GTCTGCCGGC AGCATGCATC 1980
CAAGGCCAGA GCTCAGGCCT GCAGACTGGG CTGGTGCCTC CTCCGCTTCA GGGTATGGGA 2040
GTTGGTGAAG GGGCTTTCAA AAAATAATAA GAAAAAAAG GTAAAGTCTT TGGTAGCTTC 2100
TATCCACTCA GATCCTGGAA GGCAGCAAGG TTTTGTGGAT CTAGATTCAT TAGGAATGTC 2160
TTCTTGTGAG CCAGGCCAGG ACCCGGGCTT GCCAAGAGCA GAGGCCCTCC CAGCAACCAG 2220
GATACCACCA CTTTGGGGGC TTTGTGTACA GAGGTCCGGG TCTGAGACCT CATAGGCTGC 2280
AGAAATCTGG GGCAGCCACC ATCAAGAAGC CCCTCTCAGG GGCCAGAACT CCTTTGCCAG 2340
CGTGGATTTT TCAAGTCGGG ACTGCATAAT TAAAGCAGTT GCAGTTTTAT TTTTTTTACA 2400
GCTTTTTTCC CAAAAATGAT TTGTAGTTGT GTGTGCAGCA CTTCGCCCTG ATATGTGTGC 2460
TCTACAATAA AAACCAAATC TAATATATTT TGAAAAAAA AAAAAAAA AAAA 2514

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(2) INFORMATION ON SEQ ID NO. 245:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3903 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GCAGTTGGAT CCCTGGCGGG TGGCGCCCGG CCCGGCCCGT GAGCGGCGCA CAGAATGGGC 60
 CGATGCTGCT TCTACACGGC GGGGACGTTG TCCCTGCTCC TGCTGGTGAC CAGCGTCACG 120
 CTGCTGGTGG CCCGGGTCTT CCAGAAGGCT GTAGACCAGA GTATCGAGAA GAAAATTGTG 180
 TTAAGGAATG GTACTGAGGC ATTTGACTCC TGGGAGAAGC CCCCTCTGCC TGTGTATACT 240
 CAGTTCTATT TCTTCAATGT CACCAATCCA GAGGAGATCC TCAGAGGGGA GACCCCTCGG 300
 GTGGAAGAAG TGGGGCCATA CACCTACAGG GAACTCAGAA ACAAAGCAAA TATTCAATTT 360
 GGAGATAATG GAACAACAAT ATCTGCTGTT AGCAACAAGG CCTATGTTTT TGAACGAGAC 420
 CAATCTGTTG GAGACCCTAA AATTGACTTA ATTAGAACAT TAAATATTCC TGTATTGACT 480
 GTCATAGAGT GGTCCCAGGT GCACTTCCTC AGGGAGATCA TCGAGGCCAT GTTGAAAGCC 540
 TATCAGCAGA ACCTCTTTGT GACTCACACA GTTGACGAAT TGCTCTGGGG CTACAAAGAT 600
 GAAATCTTGT CCCTTATCCA TGTTTTCAGG CCCGATATCT CTCCCTATTT TGGCCTATTC 660
 TATGAGAAAA ATGGGACTAA TGATGGAGAC TATGTTTTTC TAACTGGAGA AGACAGTTAC 720
 CTTAACTTTA CAAAAATTGT GGAATGGAAT GGGAAAACGT CACTTGACTG GTGGATAACA 780
 GACAAGTGCA ATATGATTAA TGGAACAGAT GGAGATTCTT TTCACCCACT AATAACCAAA 840
 GATGAGGTCC TTTATGTCTT CCCATCTGAC TTTTGCAGGT CAGTGTATAT TACTTTTCACT 900
 GACTATGAGA GTGTACAGGG ACTGCCTGCC TTTTCGGTATA AAGTTCCTGC AGAAATATTA 960
 GCCAATACGT CAGACAATGC CGGCTTCTGT ATACCTGAGG GAAACTGCCT GGGCTCAGGA1020
 GTTCTGAATG TCAGCATCTG CAAGAATGGT GCACCCATCA TTATGTCTTT CCCACACTTT1080
 TACCAAGCAG ATGAGAGGTT TGTTTCTGCC ATAGAAGGCA TGCACCCAAA TCAGGAAGAC1140
 CATGAGACAT TTGTGGACAT TAATCCTTTG ACTGGAATAA TCCTAAAAGC AGCCAAGAGG1200
 TTCCAAATCA ACATTTATGT CAAAAAATTA GATGACTTTG TTGAAACGGG AGACATTAGA1260
 ACCATGGTTT TCCAGTGAT GTACCTCAAT GAGAGTGTTT ACATTGATAA AGAGACGGCG1320
 AGTCGACTGA AGTCTATGAT TAACACTACT TTGATCATCA CCAACATACC CTACATCATC1380
 ATGGCGCTGG GTGTGTTCTT TGGTTTGGTT TTTACCTGGC TTGCATGCAA AGGACAGGGA1440
 TCCATGGATG AAGGAACAGC GGATGAAAGA GCACCCCTCA TTCGAACCTA AACATTGCCT1500
 TTGCTTGGTG AAGAACTGT GTGAGCTGTC CTGACCTGGA CGATGACGTG GGGAAACCT1560
 CCACCTCCTT GCAGGCTTGT TGCCTGTTGA AAGAAGGAAA AAGACACGGC GCTGGCAAGT1620
 GATAGGAACA TTCTGGCCAG AGGTTAAAGA GCAGGCTGAC ATGGCTGGCC ATTAAGCTTT1680
 ATAAATCAT GTGGGCTCTG AAATTGTTCT TTTATGTGTC TAGCAAGTAT TTAATAAAC1740
 CTTGTATAGT AAAAAAAG TTGTTGGGTG CTGGTAGCTC CAGAATTTTG TGACCACTAT1800
 TGTGGGTAAA ATGTCTCTGC ATCACTTGT AATGCTACTG GTCTAACTTC ATTCAGTATG1860
 CTTCAATCAC CGAACTTTGT GCTCAAATG CGTATATACC ATTTTATGTT GTATTCCTCC1920

ATTTCACTTG CAAAACAGAA GTAAATAAGA GTTCGGGACC CAGGGTAAAA TGGTAGCTTC1980
 ATCCAATATA TCATTCAAAT GCATCTGATT TCTAAAACAT ATTACATTTT ATGCTGATCT2040
 TCAGTTCATA ATTCTTCCAG GAAAACTCAG TCTTCCAAC GCAATAAAAT ACTGGGTAGA2100
 ATCAAATGGG AAAGGGGTTG GGTGGGGCAA TACCCATGAG TTGATAGTGA TAAGCTCCTA2160
 AGGATTTTTA ACTTGTAATT TTGTGAACGA AGAGAATGCA TAAATAATGT TGGTGAGGAT2220
 AAAGTACAGA TATTTTATGT AGAATTAATT GCTAGTTATG ATGCTTGTGG ATAGTTAACT2280
 GTTTTTTTTT TAGTCAAAAT GATCATGCTA CGAAAAGATG CTTCTGAGAG AATGTAATGA2340
 GTAACATGATT TTTCTTCTCG AGTCGCCCTT GCCAAATATG TTACTGTATT AATTAATCTA2400
 ATATTGAGTG ATTATTTGTA AAATTATGAA TATGGGAAAT CCATCTATCT ACAGCCTAAG2460
 TTACACATAA GTTTCAGAAA GTCTGATTAG ACTAAAGAGA TATTTCTTCT GGGACAGCCT2520
 TCTTCTTGGT AATTTTGAAG TTCTTTTAC AAGTTCCTTC CTCAGTTTCA GTTCTTTCCA2580
 GTGTTTTGTA GCTCACTGTC ACTCACTGAA TAGAGAAACG TGTGCCCTAT ACTTCCTGTG2640
 ACAATCATTT TGCTGACAGA ATGATGGATG TTTAAAATAT TGCACAAAGT ACTTTAAAGA2700
 AAGGTCTGTT AGGACCAGAA GCAGAGACAC CACTTTTCAA AGGACTTCTT GGTTCAGCA2760
 TAACCTAAGA CAGGGAATTG GGAGCCATCA TATGTCACAG TGTTCAGAAT TCAAGCATAT2820
 TTAAGGGCAT TTTCTTTGAT TCTCAAAGTT CAGCATTCAT TTTGAATTGA GAAGCCTATA2880
 CATTTAGCTG ACAAAGTGCT TATAGAATTT CTTAACAAC GAACCATTC AAGGATTTT2940
 TTTTGTTTAA AACTGGATTT CAATGTAAGC AAATGAAGAA AAAATATAGA TTTCAATTTCC3000
 ATAGCTTCTT ATCCCTGTAT TGAGGTAATA AATTGTTTTA CTGACAATTT TTCCTTTTCC3060
 TACACTAAAA CAATATGTGA TATATTCCC CTCTGAAGA GGCAATTCAT TAACTCTCA3120
 AATTTTCTAT AGAATCAAGA TAGAACCTTT AGATACTCCA ACTCACCAA ATGTAAAAAA3180

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ACTAACAAAA ATATTTGGTC TTCAATAATG CTAAATATCT ACATTTTATAG AATTTATCAA3240
CATTTAACTA GATAATTGGG CATGTCTTAA TTATGCATGT ACTTATCCAT ACTAATAAAA3300
TTGACAATGC TAGTGCATAC TTATTGGTTT AGTCCTATTA TCAGGATATA ATCATCTGTG3360
AGGAGGATAT TTTAAATACT GTAAATGATA ACAGTTAATG ATATACACAT TTAGACTGAG3420
TTGCACACTG GCAGGGGAGAC CAAAAACATT ACTTCCATAC TTGTGTCATG ATTCTTTTTT3480
TTTTGAGAGA GTCTCACTCT GTCGCCAGGC TGGGAGTACA GTGGCATGAT CTCGGCTCAC3540
TGCAACCTCT GCCACCCAG GTCCAAGTGA TTCTTCTGCC TCAGTCTCCC GAGTAGCTGG3600
GACTACAGGC ACCCACGAGC ATGCCTGGCT AATTTATGTA TTTTATAGTAG AGACGGGGTT3660
TCACCATGTT GGCCAAGCTG GTCTCAAACCT CCTGACCTCA AGTGATCCAC CCACCTCAGC3720
CTGTCGAAGT GCTGGGATTA CAGGTGTGAG CCACTGCGCC CACCTTCTAT TTTCATCTTC3780
TTTTTAAGGA ATTAATTATT TGAATATGGC AAACATCCAC ATGGGGCCTA AAGTCAAATA3840
ATGTAAAGCG ATACATTAAA AGGGCTTTAC TTCCACCTC TTTAGGTCTT AATTCAGTCA3900
GTT

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(2) INFORMATION ON SEQ ID NO. 246:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1730 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

GCATTTCTGC	CATCGCCAC	CGTGGCGGCA	CAAGCGGCAG	CCCGAGAACA	CGCTGGCGGC	60
CATTCGGCAG	CTAAGAATGG	AGCAACAGGC	GTGGAGTTGG	ACATTGAGTT	TACTTCGGAC	120
GGGATTCCTG	TCTTAATGCA	CGATAACACA	GATAGATAGGA	CGACTGATGG	GACTGGGCGA	180
TTGTGTGATT	TGACATTTGA	ACAAATTAGG	AAGCTGAATC	CTGCAGCAAA	CCACAGACTC	240
AGGAATGATT	TCCCTGATGA	AAAGATCCCT	ACCCTAAGGG	AAGCTGTTGC	AGAGTGCCTA	300
AACCATAACC	TCACAATCTT	CTTTGATGTC	AAAGGCCATG	CACACAAGGC	TACTGAGGCT	360
CTAAAGAAAA	TGTATATGGA	ATTTCTCTCA	CTGTATAATA	ATAGTGTGGT	CTGTTCTTTC	420
TTGCCAGAAG	TTATCTACAA	GATGAGACAA	ACAGATCGGG	ATGTAATAAC	AGCATTAACT	480
CACAGACCTT	GGAGCCTAAG	CCATACAGGA	GATGGGAAAC	CACGCTATGA	TACTTTCTGG	540
AAACATTTTA	TATTTGTTAT	GATGGACATT	TTGCTCGATT	GGAGCATGCA	TAATATCTTG	600
TGGTACCTGT	GTGGAATTTT	AGCTTTCTCT	ATGCAAAAGG	ATTTTGTATC	CCCGGCCTAC	660
TTGAAGAAGT	GGTCAGCTAA	AGGAATCCAG	GTTGTTGGTT	GGACTGTTAA	TACCTTTGAT	720
GAAAAGAGTT	ACTACGAATC	CCATCTTGGT	TCCAGCTATA	TCACTGACAG	CATGGTAGAA	780
GACTGCGAAC	CTCACTTCTA	GACTTTTACG	GTGGGACGAA	ACGGGTTTCA	AAACTGCCAG	840
GGGCCTCATA	CAGGGATATC	AAAATACCCT	TTGTGCTAGC	CCAGGCCCTG	GGGAATCAGG	900
TGACTCACAC	AAATGCAATA	GTTGGTCACT	GCATTTTAC	CTGAACCAAA	GCTAAACCCG	960
GTGTTGCCAC	CATGCACCAT	GGCATGCCAG	AGTTCAACAC	TGTTGCTCTT	GAAAATCTGG	1020
GTCTGAAAAA	ACGCACAAGA	GCCCCTGCCC	TGCCCTAGCT	GAGGCACACA	GGGAGACCCA	1080
GTGAGGATAA	GCACAGATTG	AATTGTACAA	TTTGAGATG	CAGATGTAAA	TGCATGGGAC	1140
ATGCATGATA	ACTCAGAGTT	GACATTTTAA	AACTTGCCAC	ACTTATTTCA	AATATTTGTA	1200
CTCAGCTATG	TTAACATGTA	CTGTAGACAT	CAAACCTGTG	GCCATACTAA	TAAAATTATT	1260
AAAAGGAGCA	CTAAAGGAAA	ACTGTGTGCC	AAGCATCATA	TCCTAAGGCA	TACGGAATTT	1320
GGGGAAGCCA	CCATGCAATC	CAGTGAGGCT	TCAGTGATCA	GCAACCAAAA	TGGTAGGGAG	1380
GTCTTGAAGC	CAATGAGGGA	TTTATAGCAT	CTTGAATAGA	GAGCTGCAAA	CCACCAGGGG	1440
GCAGAGTTGC	ACTTTTCCAG	GCTTTTTAGG	AAGCTCTGCA	ACAGATGTGA	TCTGATCATA	1500
GGCAATTAGA	ACTGGAAGAA	ACTTCCAAAA	AGATCTAGGG	GTATGCTCAT	GGTGCAAAGT	1560
GGGGGAACATA	AACTCTTAGG	GGAGAAGAGG	GGGTGACCCG	CAAAAGAGAC	GAGATTAGAG	1620
GGAACGAGAG	GGGGAAGCCG	GAGAGTCCAG	GAAATAAGGA	GGTGAAGAAA	GAAGGTTGTT	1680
TAAGGCGAGC	TGGGGAAGTT	GGAAGCCCGA	AACTTGAAAG	GAGGATAAAA		1730

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3439 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

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CAGATTTTGC CGGCTTTTAT CCTTTTATTT AACGGATTGA AAAGAGCATA TGCCTGCCAT 60
GCAGAACATG AAACCGAGGA ACTGGGGAGT GATGAAGATG ATATTGATGA AGATGGGCAA 120
GAATATTTGG AGATTCTGGC TAAGCAGGCT GGTGAAGATG GAGATGATGA AGATTGGGAA 180
GAAGATGATG CTGAAGAGAC TGCTCTGGAA GGCTATTCCA CAATCATTGA TGATGAAGAT 240
AACCCTGTTG ATGAGTATCA GATATTTAAA GCTATCTTTC AAATATTCA AAATCGTAAT 300
CCTGTGTGGT ATCAGGCACT GACTCACGGT CTTAATGAAG AACAAAGAAA ACAGTTACAG 360
GACATAGCAA CTCTGGCTGA TCAAAGAAGA GCAGCCCATG AATCCAAAAT GATTGAGAAG 420
CATGGAGGAT ACAAATTCAG TGCTCCAGTT GTGCCAAGTT CTTTCAATTT TGGAGGCCCA 480
GCACCAGGGA TGAATTGAGT TATCTCTTTC TTTCCTGCTG TGTGCTTGTA GTGAAGAGCT 540
TGTGTTCCCTC CTAGTAGTGG TTCCAGAACT GGTTTCATGTT ATCTATTCTA AACTAATAAT 600
CAATAGATGG ACAAAGAAA CAACAACCCC AGGAGATGGG ACCTGATCAT GCAACCTGGC 660
ACTGGAAGAG AAATCAGCGG GATTTTGGGG GTGGGGGGGA TGGGAGGTAC CTTAGAGGGA 720
GTATTTTCTT TATTTTTTGA AGAAAGTAAG ATCCTGACTC TGAAGCTTCA AAGTGACACT 780
GTGGAAATCT GAAACGAGGG GATGTCATGA AGGCAGCTTT TCTTTTCTG AGGAAAAAAT 840
AGGCATGGGC TACAGGACTA TTAAAATGT CTCATTTACA GTATAAACT CAAAGGTAGA 900
TGTAATTTTT ACACCTATGA GTATTTGTCC AATTTCTGTC TCTTCCTCAC CATTGGGTAT 960
CTATTCCTTA TATGTAAATA AGATAAGGTC ATCTGATAGC CTTATTCAGT CTTTCATCATT 1020
TTCATCATTG TTCTATGTA GATTATTGGA CATTATTGT AGCACTACAT AACTGATTAT 1080
AAAAATCTGT AAATGAATTA GCACCTTCAT ATTGAAACAA GCCTGCTAGC CTATGTATAA 1140
AATAGCAAAA TGTTTGCTGT TTATAAAAAG ATGTAATGGG GTGGGGGGCA GGGGTAATTT 1200
CAAGTTATTA ATTTAAAAAT GAACTAGCAA TTTTGTACCT GGTGACTTTG TGGTGCACTC 1260
ACCTCTGATA GTGACTTGAA TTCGGTATGT AAAAAGGGGT TAGTGGTATT TCATTGCTGC 1320
TAAAAATGAC AACTCCCTCT GTGTCCTGTT TTTCTTAAAG CTGTCAGTGT ACAAGTGGGT 1380
ATTTGAATAC CAGACCTTAC TGTAATAAAT AAAAAGGTG GTATCTAGAG CATGTAAATT 1440
GGATATAAAG TTCTGCTCTT AAAGAGTTGA TCTAAGAGTA TGGCTAAACA TCTATATATG 1500
CAATCTATTA AAAGAACTTA ATTCGGCTAT TATGTCTTGA TTTGATTGCA GTTTTTTCT 1560
AATTATAACA AATTTTCTCT CATTGGCCTG TTTTAAATCC TGTGCCTAGA AGGAGTACAA 1620
AATGCACACT TTACAAAATT GATATTTAAC ACTTACCCAC TCCCCTTTCC CCATCTCTTC 1680
TACCGCTCTT GTTGATCGTG GTATCTGATC TTGACTAGAT AGGCTGAAGG CACATGGTTC 1740
CCTCCAAAAA CCACTATTGA TACCACTACA AAAACAAGCC AGCAAAAAGA TACTGTAGAG 1800
AGGTTGGCTT GCTTCCCTCT CTTCCCTAAT GCATGTTGAA AAATAAGCCG TTATTGATCT 1860
TAAACATCGG TCAGATGAGT CATACATTGG GTTATTTTTT ATATACATGT ATACACAAAA 1920
TATTTCAAAT TGAAAGCAAC ATCTTAATGG ATTCAAAAC ATTACAAGCT GTTGTCTAAA 1980
ACAGGTGAGA AAAAAATTTA TAACTGTAAA AACAAATGCA CATATTGATA TTTAAAATGC 2040

```

GTCTTTGTTA ATGGCACATA TTAGCATAAA TCACTTTTGT AAATGTAAGC TTTCTTTTTT3060
 TTTCTTGAAA AAGCCTTTCT ATTTATCAGT ATTAAATAAA GGAAGTTAAT CTGTTTCTCT3120
 GCAGGTAATA AAATAGTGAC ACACTGTATT AAGATAGTGA CTGCTATACT CAACTCTGGA3180
 AGAGACTAGA GTATAGAGCA TGAGTGGCAA AACCACAGCC CTTGGGCCAT ATGCTGCTAT3240
 TCAGTCCCAG ATGTAGCCCC TGAAGCAAGC ATAAAGAAAA ATGAATTAAA AATTAAATTA3300
 ATATGGAAAG TTAAAAAATG GATTACATTA GTATGACTAA ACCATGTCTT TGGCAAAGAT3360
 CTAAACACAAT GTCTTAAGTA TAATAGGTAG TCTCTGTTTG TAAAATAAAT GACTTAAATT3420
 TAAAACATCA AAAAAAAAAA

(2) INFORMATION ON SEQ ID NO. 248:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 378 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
SCSSPSCHRG HERFRIASAC LDELSCEFL L AGAGGAGAGA APGPHLP PRG SVPGDPVRIH 60
CNITESYP AV PPIWSVESDD PNLA AVLRL VDIKKGNTLL LQHLKRIISD LCKLYNLPQH 120
PDVEMLDQPL PAEQCTQEDV SSEDEDEEMP EDTEDLDHYE MKEEPAEGK KSEDDGIGKE 180
NLAILEKIKK NQRQDY LNGA VSGSVQATDR LMKELRDIYR SQSFKGGNYA VELVND SLYD 240
WNVKLLKVDQ DSALHNDLQI LKEKEGADFI LLNFSFKDNF PFDPPFVRV V SPVLSGGYVL 300
GGGAICMELL TKQGWSSAYS IESVIMQISA TLVKGKARVQ FGANKSQYSL TRAQQSYKSL 360
VQIHEKNGWY TPPKEDG* 378
```

(2) INFORMATION ON SEQ ID NO. 249:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 281 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```
AVGSAALFKD GGGGTSAAEA GAAGQRLRSV NCLAYDEAIM AQQDRIQQEI AVQNPLV SER 60
LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSHL EALLDDSKEL 120
QRFKA VSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL 180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVSI 240
QVEYMDRGEG GTTNPHIFPE GSEPKVYLLY RPGHYDILYK * 281
```


(2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 245 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```
DHLQPQKNLC TCLAPGRGGQ QGSSGLEPAL FVEDIVVSRP VEKVDLGLGA LREDVRIGGA 60
ALAAVHVLHL DGHAEGIGQR NDVDVVALLA HGLHLLLAEL LDSPSTLDEV LEELALALQV 120
ARGEQPQVDH KVVGGALVIE GGQQVGDRGL LLHLLNQVHE RVVEILNCEF SEALGHQVFL 180
ALGRHSLEPL QLLAVIQQCL QVGESESPIE TVAVRPGLAD VRVLFVEVLD LLLIDVVIFS 240
ELLV* 245
```

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 294 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```
MLAARLVCLR TLPSRVFHPA FTKASPVVKN SITKNQWLLT PSREYATKTR IGIRRGRTGQ 60

ELKEAALEPS MEKIEFKIDQM GRWFVAGGAA VGLGALCYYG LGLSNEIGAI EKAVIWPQYV 120
KDRIHSTYMY LAGSIGLTAL SAIAISRTPV LMNFMMRGSW VTIGVTFAAM VGAGMLVRSI 180
PYDQSPGPKH LAWLLHSGVM GAVVAPLTIL GGPLLIRAAW YTAGIVGGLS TVAMCAPSEK 240
FLNMGAPLGV GLGLVFVSSL GSMFLPPTTR GWCHSLLSGN VRWISSFQHV PSV* 294
```

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 564 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

MERELNHEKE	RCDQLQAEQK	GLTEVTQSLK	MENEEFKKRF	SDATSKAHQL	EEDIVSVTHK	60
AIEKETELDS	LKDKLKKAQH	EREQLECLK	TEKDEKELYK	VHLKNTEIEN	TKLMSEVQTL	120
KNLDGNKESV	ITHFKEEIGR	LQLCLAEKEN	LQRTFLLTTS	SKEDTCFLKE	QLRKAEQVQ	180
ATRQEVVFLA	KELSDAVNVR	DRTMADLHTA	RLENEKVKKQ	LADAVAECLK	NAMKKDQDKT	240
DTLEHELRE	VEDLKLRLQM	AADHYKEKFK	ECQRLQKQIN	KLSDQSANN	NVFTKKTGNQ	300
QKVNDASVNT	DPATSASTVD	VKPSPSAAEA	DFDIVTKGOV	CEMTKEIADK	TEKYNKCKQL	360
LQDEKAKCNK	YADELAKMEL	KWKEQVKIAE	NVKLELAEVQ	DNYKELKRSL	ENPAERKMED	420
GADGAFYPDE	IQRPPVRVPS	WGLEDNVVCS	QPARNFSPRD	GLEDSSEDSKE	DENVPTAPDP	480
PSQHLRGHGT	GFCFDSSFDV	HKKCPLCELM	FPPNYDQSKF	EEHVESHWKV	CPMCSEQFPP	540
DYDQQVFERH	VQTHFDQNVL	NFD*				564

(2) INFORMATION ON SEQ ID NO. 253:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 250 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

WTGTGRGAVA	IMADPDPRYP	RSSIEDDFNY	GSSVASATVH	IRMAFLRKVY	SILSLQVLLT	60
TVTSTVELYF	ESVRTFVHES	PALILLFALG	SLGLIFALTL	NRHKYPLNLY	LLFGFTLLEA	120
LTVAVVVTFY	DVYIILQAFI	LTTTVFFGLT	VYTLQSKKDF	SKFGAGLFAL	LWILCLSGFL	180
KFFFYSEIME	LVLAAAGALL	FCGFIIYDTH	SLMHKLSPEE	YVLAAISLYL	DIINLFLHLL	240
RFLEAVNKK*						250

(2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 152 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

PKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60
TWNGMRKRG GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFV GRLPIHPVEI 120
VAGLLGGVK PVSDRQAGKG LGDGGCGRER V* 152

```

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 151 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60
YESPGRRGDS GSWPGPGRQV ALEMKGKCLCR GAELSLCFSF FPLLLPLHTP VAGRNLFPE 120
SLGVPPFLPH PGGTPRAPGL FLLLFSEWAV * 151

```

(2) INFORMATION ON SEQ ID NO. 256:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 276 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

GRPGQSPAGA	EEPGPRDSSA	VITQISKEEA	RGPLRGKGDQ	KSAASQKPRS	RGILHSLFCC	60
VCRDDGEALP	AHSGAPLLVE	ENGAIPKTPV	QYLLPEAKAQ	DSDKICVVID	LDETLVHSSF	120
KPVNNADFII	PVEIDGVVHQ	VYVLKRPHVD	EFLQRMGELF	ECVLFTASLA	KYADPVADLL	180
DKWGAFRARL	FRESCVFHRG	NYVKDLSRLG	RDLRRVLILD	NSPASVVFHP	DNAVPPVASWF	240
DNMSDTELHD	LLPFFEQLSR	VDDVYSVLRQ	PRPGS*			276

(2) INFORMATION ON SEQ ID NO. 257:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 139 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

MFYLAAAVSD	FYVPVSEMPE	HKIQSSGGPL	QITMKMVPKL	LSPLVKDWAP	KAFIISFKLE	60
TDPAIVINRA	RKALEIYQHQ	VVVANILESR	QSFVFIIVTKD	SETKLLLSEE	EIEKGVEIEE	120
KIVDNLQSRH	TAFIGDRN*					139

(2) INFORMATION ON SEQ ID NO. 258:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

PYRQGCPGAA	GQAPGAPPGS	YYPGLPSGTP	GGPYGGAAPG	GPYGQPPPSS	YGAQQPGLYG	60
QGGAPPNVDP	EAYSWFQSV	SDHSGYISM	ELKQALVNC	WSSFNDETC	DMFDKTK	120
SGRIDVYGFS	ALWKFIQQW	NLFQQYDRD	SGSISYTEL	QALSQMGYN	SPQFTQLLV	180
RYCPRSANPA	MQLDRFIQV	TQLQVLTEA	REKDTAVQN	IRLSFEDFV	MTASRML*	238

(2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

TNICLLSGAS	PKVTNGWAQI	NFSFASHRVA	HCGKPELVRT	PVCVFLIHTN	HNKQVCTHLY	60
EPHAKTRHSQ	RSVTRVQQRN	SRFDQNRPC	LLNCQLPLKN	LQKKGHYKNS	*	111

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

FVKILKFGPL RIILNEIYRL TCENIFHRLS LGLFIRKLFV CPPVGTFGYL ILPFQIVKAH 60
RGVFWNHLLS HFLKSYSIVS VNI*                                           84

```

(2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

PQTTQCVRRR GLWVNSHIHT QGRGKHTQVQ SSQWCRPDLL SRGCYGCPSA SPEQPGQPAP 60
PPRLXQEGEL CPGEETDRLG DKTPIAGTCT AAATAPRTGH GDGTGREPHC PLSVCLWFCP 120
GPAHLEPRQT GGIEQGPQPD SPLARCDWKR LMPGQHQAFC KSQSQAESA STACAVAPQD 180
EVTSRTGGFM QTHRHC*                                                  197

```

(2) INFORMATION ON SEQ ID NO. 262:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```
DQLGSGGHFS LHRLPEQTEE SSLIVAEPST SPSAVSVCLH KPSCPGRDFI LRSHSTGRAG 60
TFCTLALGLA EGLVLPWHQP LPVTSGQRAV WTWALLNATC LPGLQVGRTR TEPQAHTEGA 120
VWLPAACPIPM PRPRGCGCCC ACPCDGSLSV QPVSFLPRAE LPFLXESGRR CRLSWLLWGS 180
RGTAITPPGQ *
```

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 245 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```
EKMEAFGEGA GWEDFFSTQT LTFQSILQMK NADYFSNYVT EDFTTYINRK RKNNCHGNHI 60
EMQAMAEMYN RPVEVYQYST EPINTFHGIH QNEDEPIRVS YHRNIHNSV VNPKNKATIGV 120
GLGLPSFKPG FAEQSLMKNA IKTSEESWIE QQMLEDDKRA TDWEATNEAI EEQVARESYL 180
QWLRDQEKQA RQVRGPSQPR KASATCSSAT AAASSGLEEW TSRSRQGVQ PRHLSTLSCM 240
LNWA*
```

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 221 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
GFRPARCDPV PLPTTRSVAG LPVGRVRQLS RPLLGPDTGS VANIFKGLVI LPEMSLVIRN    60
LQRVIPIRRA PLRSKIEIVR RILGVQKFDL GIICVDNKNI QHINRIYRDR NVPTDVLSFP    120

FHEHLKAGEF PQPDFPDDYN LGDIFLGVEY IFHQCKENED YNDVLTVTAT HGLCHLLGFT    180
HGTEAEWQQM FQKEKAVLDE LGRRTGTRLQ ALTRGLFGGG *                          221
```

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 109 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
FFFLRSFVIY LCATPAPRSL HPSRVPLSEG TRPSAPSEEA PGQGLQPGPR ASAQLVQHRL    60
LLEHLLPLC LRAVCESQQV TESVGGRHSQ DVIVIFIFT LMEDILHS*                  109
```

(2) INFORMATION ON SEQ ID NO. 266:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 372 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

MSFRKVNIII	LVLAVAFLL	VLHHNFLSLS	SLLRNEVTDS	GIVGPQPIDF	VPNALRHAVD	60
GRQEEIPVVI	AASEDRLGGA	IAAINSIQHN	TRSNVIFYIV	TLNNTADHLR	SWLNDSLKLS	120
IRYKIVNFD	KLLEGKVKED	PDQGESMKPL	TFARFYLPIL	VPSAKKAIYM	DDDVIVQGDI	180
LALYNTALKP	GHAAAFSEDC	DSASTKVIR	GAGNQYNYIG	YLDYKKERIR	KLSMKASTCS	240
FNPGVFEVANL	TEWKRONITN	OLEKWMKINV	EEGLYSRTLA	GSITTPPLLI	VFYQQHSTID	300
PMWNVRHLGS	SAGKRYSPQF	VKAAKLLHWN	GHLKPWGRTA	SYTDVWEKWKY	IPDPTGKFNL	360
IRRYTEISNI	K*					372

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

MCLLSQQSPA	ASSLEGAIWR	RAGTQTRALD	AILYHPQQSH	LVGSTALGLT	LPLLYPREPE	60
AGGWKDPVAG	GG*					73

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 137 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

VPPCPQLREL	CPGVNNQPYL	CESGHCCGET	GCCTYYYELW	WFWLLWTVLI	LFSCCCAFRH	60
RRAKLRLLQQ	QRQVEINLLA	YHGACHGAGP	FPTGSLDLR	FLSTFKPPAY	EDVVHRPGTT	120
SPPLYCGPKA	PLEVVSS					137

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 309 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

KHATEQEKTE	EGLGPNVKGI	VTMLMLMLLM	MFAVHCTWVT	SNAYSSPSVV	LASYNHDGTR	60
NILDDFREAY	FWLRQNTDEH	ARVMSWWDYG	YQIAGMANRT	TLVDNNTWNN	SHIALVGKAM	120
SSNETAAYKI	MRTLDVDYVL	VIFGGVIGYS	GDDINKFLWM	VRIAEGEHPK	DIRESDYFTP	180
QGEFRVDKAG	SPTLLNCLMY	KMSYYRFGEM	QLDFRTPPGF	DRTRNAEIGN	KDIKFKHLEE	240
AFTSEHWLVR	IYKVKAPDNR	ETLDHKPRVT	NIFPKQKYL	KKTTRKRGY	IKNKLVFKKG	300
KKISKKTIV*						309

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

IPEDPHIDES	KAKHQAIIMS	TSLRVSPSIH	GYHFDTASRK	KAVGNIFENT	DQESLERLER	60
NSGDKKAEER	AKIIFAIDQD	VEEKTRALMA	LKKRTKDKLF	QFLKLRKYSI	KVH*	114

(2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

QMQHFAATLQ ASLLSGLQRL ERDRDWKGTR TEQTGYKDSK QFHALCCYRG EQNAFSKDLK 60
 TLPSLQERID ADRAWTDVM RTKENRWLEM TFIQGHFVRP * 101

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

PRIPVTLNMK MVMPSQCGLD *

21

(2) INFORMATION ON SEQ ID NO. 273:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CPPVKALIEH	EMKNGIPANR	IVLGGFSQGG	ALSLYTALTC	PHPLAGIVAL	SCWLPLHRAF	60
PQAANGSAKD	LAILQCHGEL	DPMVPVREGA	LTAEKLRSVV	TPARVQFKTY	PGVMHSSCPQ	120
EMAAVKEFLE	KLLPPV*					137

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

MWVLKLDLDRNT	MNVKIPPIFC	SKKKNPKNKK	TNKKPRMFFG	ITEISQTWVF	SYSLCTFFQV	60
LCFACSTDCV	ILIFIDSSLA	MQYPCLTHRC	L*			92

(2) INFORMATION ON SEQ ID NO. 275:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```
ETIADNALPS TEITLESPLL GSFDCLTQDV LCHSEVFIWG RSLYGDVNDV VSGLCITSHW 60
SETPVCQAWI LHCKT* 76
```

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
GGKEKTKKIQ LRNRTMIOHL QKASSISLKK ATDCASAGSE KGWAAGTAAS WVTRQQSQRL 60
EVRLRTPLWP EHKRHWCKL SVTWPSFLSS ISPNICAHPE ELSGNSRVRA GRRGERTKRE 120
```

(2) INFORMATION ON SEQ ID NO. 277:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
VAPFPIPTQE HRGGGEGRLS LSKSSYLHFR RKAETQSRLY INCLADRVTK THWSTCAFSS 60
LCPSLIQTAT CQSPATLKTH GOLPGFTKLT AFLHKVKT TT ASVCGPSATT KLS 113
```

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PYDPACLLIF SLPLPFLSLS SRSHLPGLKY FVGIAYYIIL ADEPQDNVYT HTHTYHTKS 60
 QLLKSGLGIR LLCPVKNSCT EVIVT* 86

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

NSFKVVKKLA TTWSLSIKRK QGKQTHSLDQ KKLDQVHWNQ SVTTQVTMTS VQEFFTGHRS 60
 LIPSPLFNS* 70

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 594 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

VSEKCRIDTE	ILPSLFMRCT	TDLNRKDKFP	AITHLKFLAR	DMSEQVLLCA	SSQTSSIVEC	60
WSLRKEGLPV	NNIFQQISPV	VGDKQPTILK	WRILSATNDL	DRVSAVALPK	LPISLTNTDL	120
KVASDTQFYP	GLGLALAFHD	GSVHIVHRLS	LQTMVAFYSS	AAPRPVDEPA	MKRPRTAGPA	180
VHLKAMQLSW	TSLALVGIDS	HGKLSVLRLS	PSMGHPLEV	LALRHLLFLL	EYCMVTGYDW	240
WDILLHVQPS	MVQSLVEKLH	EEYTRQTAAL	QQVLSTRILA	MKASLCKLSP	CTVTRVCDYH	300
TKLFLIAISS	TLKSLLRPHF	LNTPDKSPGD	RLTEICTKIT	DVDIDKVMIN	LKTEEFVLDM	360
NTLQALQQLL	QWVGDFVLYL	LASLPNQGSL	LRPGHSFLRD	GTSLGMLREL	MVVIRIWGLL	420
KPSCLPVYTA	TSDTQDSMSL	LFRLLTKLWI	CCRDEGPASE	PDEALVDECC	LLPSQLLIPS	480
LDWLPASDGL	VSRLQPKQPL	RLQFGRAPTL	PGSAATLQLD	GLARAPGQPK	IDHLRRLHLG	540
ACPTEECKAC	TRCGCVTMLK	SPNRTTAVKQ	WEQRWIKNCL	CGGLWWRVPL	SYP*	594

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 293 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

LRGTRHQSPP	HRQFLIQRCS	HCFTAVVLLG	DLSMVTQPHL	VQALHSSVGQ	APRCSLRRWS	60
ILGWPGALAR	PSSCRVAALP	GSVGARPNCR	RRGCLGCRRL	TRPSLAGSQS	RLGISSWLGS	120
RQHSSTSASS	GSLAGPSSRQ	QIQSLVSRRK	SRDMLSWVSE	VAVYTGRQLG	FRRPQMRMTT	180
INSRSMPSEV	PSRRKLWPGL	SREPWLGRLA	SRYSTKSPTH	CKSCCSACSV	FMSSTNSSVL	240
RLIMTLMST	SVILVQISVS	RSPGLLSGV	RKWGRSSDFR	VELMAMRKSL	VW*	293

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 173 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

TPALRARSILR	DRCARAPCPH	GGQQRRRRRL	NAEGAEGARG	GGSSYSEMAE	TVADTRRLIT	60
KPQNLNDAYG	PPSNFLEIDV	SNPQTVGVGR	GRFTTYEIRV	KTNLPFIKFK	ESTVRRRYS	120
FEWLRSELER	ESKVVVPPLP	GKAFLRQFLL	EEMMEYLMIT	LLRKENKGWS	SL*	173

(2) INFORMATION ON SEQ ID NO. 283:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 107 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

NYLGRFQPQW	FNDNKTTKHG	TSNSLIKLLS	HLFHRMMRFF	LFTVSHQGKK	NPPTSCLFFF	60
LMPGISIHCL	FKRPMQKKVD	KALAQELGLP	VVVPGLPCWG	VPKSV*		107

(2) INFORMATION ON SEQ ID NO. 284:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 105 amino acids
 (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

MGNFFFFEPG TCYVAQAGLE LLNSSDPLTS ASQIAETTGT HHCTWLKTIF LKNKSTALHL    60
YLLVSLQFKH TINDYNILFK AGRSGSWLQL EQFITSGYLR ARKIQ                    105

```

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

TGMGGGSGCR ELLCPCKGAE TPVELRKSDG IYRVLGKPWL CLHHGERPWA GSPPSCRSVR    60
LDADGGSDQL ASVSLRHEAA FSSGFQSHSG LPMADRVAKV RNGKCIAYYL PSPTKQIT*    119

```

(2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

YANQSSSLRF KIKYKLLCFS THSGSIVPEP DCYFFILNII FPHLICLPLI HRHLEKEMGG 60
CLLSLSLCFV PVVRLAASVA RWAWLEPWVR QVAGGDRERL RGKWWHLLL* 110

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

SQLLGRLRQE NHLNSGGRGC SELRSCHCTP AWATRVKLRL KKKKKEMFFI FFMLSIQALF 60
HGQQVIFHNV DFPK* 75

(2) INFORMATION ON SEQ ID NO. 288:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RRGFLHVGQA GLEFLTSGDP PASATQSAGI TGISHRERPI LLFIYFLRWS LALFRDLRPL 60
QPSPLQF 67

(2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

STRPRERRNR SVDECQLINV KXRHLVCLX CFCLYXQPDV VSXEYKXWGL LPQXLFXISX 60
EKKNDRXXGX IRRXARFXST NXNX* 85

```

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

MSXXDTXWCV XAVFAFTXNP TVFHXTNXG XFYPXLSSXL VKKKKMIGXX XEFXGKPXXQ 60
ALXKIXSWXX LTSLPXX* 78

```

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RAASGRSGSS	VRMSAPRSRP	ASMRWCPAPR	RACTTSTRWT	GPPCATSTSS	ARATRTGPSC	60
RSAGRARSAS	YPPGDVDEIP	DWVHQLVIQK	LVEHRVIEG	FVNSAVINDY	QPGGCIVSHV	120
DPIHIFERPI	VSVSFFSDSA	LCFGCKFQFK	PIRVSEPVLS	LPVRRGSVTV	LSGYAADEIT	180
HCIRPQDIKE	RRAVIILRKT	RLDAPRLETK	SLSSSVLPSS	YASDRLSGNN	BDPALKPKRS	240
HRKADPDAAH	RPRILEMDKE	ENRRSVLLPT	HRRRGSFSSE	NYWRKSYESS	EDCSEAAGSP	300
ARKVKMRRH*						310

(2) INFORMATION ON SEQ ID NO. 292:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 192 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SCLPEDDDCS	ALLDVLRPYA	VSDFISSIST	EHSHASPAHR	QGKHWFHPN	RLELELAEEA	60
QRRVAKEGHG	HDGALEDVDG	VHVGHDAAG	LVVVDDRAVD	EALGDDAVLH	QLLDHQLMHP	120
VRDLVDVARR	VRGAPGPARR	SAAGPRTCSP	RRRSTCCAGG	PGPPCARCTG	PSRRGTPPHR	180
CGPRSWSTHP	D*					192

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 479 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

MGRCCFYTAG	TLSELLLVT	VTLLVARVFQ	KAVDQSIEKK	IVLRNGTEAF	DSWEKPPLPV	60
YTQFYFFNVT	NPEEILRGET	PRVEEVGPYT	YRELNRKANI	QFGDNGTTIS	AVSNKAYVFE	120
RDQSVGDPKI	DLIRTLNIPV	LTVIEWSQVH	FLREIIEAML	KAYQQKLFVT	HTVDELLWGY	180
KDEILSLIHV	FRPDIPYFG	LFYEKNGTND	GDYVFLTGED	SYLNFTKIVE	WNGKTSLDWW	240
ITDKCNMING	TDGDSFHPLI	TKDEVLYVFP	SDFCRSVYIT	FSDYESVQGL	PAFRYKVPPE	300
ILANTSDNAG	FCIPEGNCLG	SGVLNVSICK	NGAPIIMSFP	HFYQADERFV	SAIEGMHPNQ	360
EDHETFDV	PLTGIILKAA	KRFQINIYVK	KLDDFVETGD	IRTMVFPVMY	LNESVHIDKE	420
TASRLKSMIN	TTLIITNIPY	IIMALGVFFG	LVFTWLACKG	QGSMDEGTAD	ERAPLIRT*	479

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 267 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AFLPSPTVAA	QAAAREHAGG	HSAAKNGATG	VELDIEFTSD	GIPVLMHDNT	VDRTTDGTGR	60
LCDLTFEQIR	KLNPAANHRL	RNDFFDEKIP	TLREAVAEC	NHNLTIFFDV	KGAHAKATEA	120
LKKMYMEFPQ	LYNNSVVCSE	LPEVIYKMRQ	TDRDVITALT	HRPWSLSHTG	DGKPRYDTFW	180
KHFIFVMMDI	LLDWSMHNIL	WYLCGISAF	LQKDFVSPAY	LKKWSAKGIQ	VVGWTVNTFD	240
EKSYYESHLG	SSYITDSMVE	DCEPHF*				267

(2) INFORMATION ON SEQ ID NO. 295:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 166 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

QILPAFILLF	NGLKRAYACH	AEHETEELGS	DEDDIDEDGQ	EYLEILAKQA	GEDGDDDEDWE	60
EDDAEETALE	GYSTIIDDED	NPVDEYQIFK	AIFQTIQNRN	PVWYQALTHG	LNEEQRKQLQ	120
DIATLADQRR	AAHESKMIEK	HGGYKFSAPV	VPSSFNFGGP	APGMN*		166

WO 99/46375

PCT/DE99/00722

Claims

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, characterized in that it is expressed elevated in normal prostate tissue.

4. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as a vehicle for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 2500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 150 to 2000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody which is directed against a polypeptide or a fragment which by the nucleic acids of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. A protein according to claim 20, wherein it originates from a phage display.

23. Polypeptide partial sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114,

116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

24. Polypeptide partial sequences according to claim 22, with at least 80% homology to these sequences.

25. Polypeptide partial sequences according to claim 22, with at least 90% homology to these sequences.

26. Use of polypeptide partial sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as tools for finding active agents against prostate cancer.

27. Use of nucleic acid sequences according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for expression of polypeptides that can be used as tools for finding active agents against prostate cancer.

28. Use of nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 in sense or antisense form.

29. Use of polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer.

30. Use of polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq.

ID No. 248-295 to produce a pharmaceutical agent for treatment of prostate cancer.

31. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

32. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

34. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, obtainable from cDNAs of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

35. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

36. Use according to claim 34, wherein the regulatory element is a suitable promoter and/or enhancer.

37. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 400 to 1900 bp.

Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue
-50,000 individual ESTs

Tumor tissue
-50,000 individual ESTs

Priority list
High

Prostate
Breast
Ovary
Bladder
Uterus

Iterative assembling
with
increasing mismatch

Low

-8,000 contigs
+
-25,000 singletons

-8,000 contigs
+
-25,000 singletons

Comparison of databases

normal tissue-
specific
(expected: 100-500)

nonspecifically
expressed genes

tumor tissue-
specific
(expected: 100-500)

Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)

Systematische Gen-Suche in der Incyte LifeSeq Datenbank

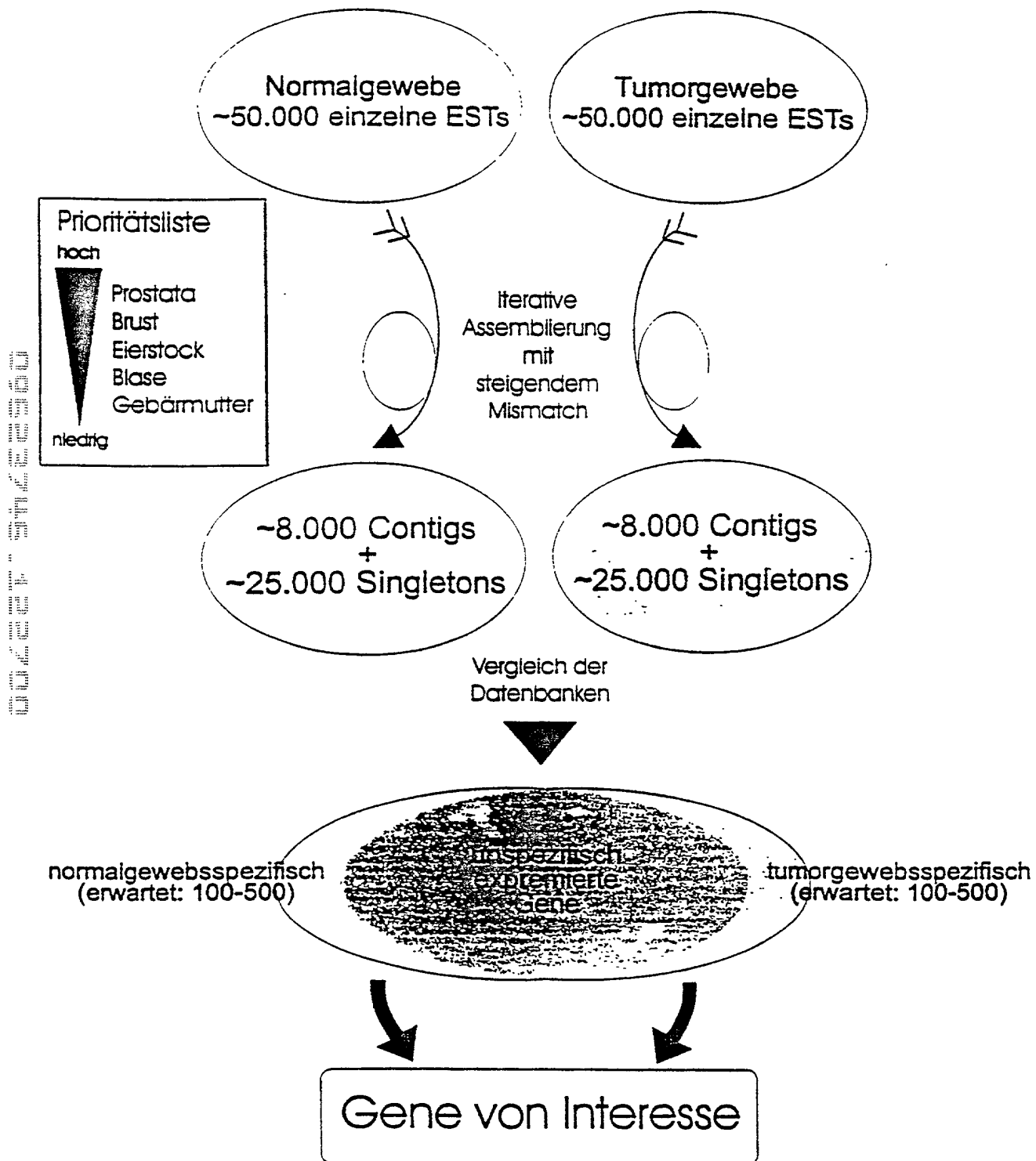


Fig. 1

09/623746

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Principle of EST Assembly

-50,000 ESTs per tissue

Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Singletons

Contigs increasing in
number and length

Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 contigs

-25,000 other
singletons

-30,000 consensus-
sequences per tissue

Figure 2a

REPLACEMENT PAGE (RULE 26)

Prinzip der EST-Assemblierung

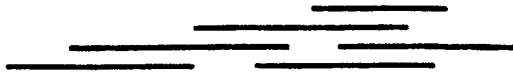
~50.000 ESTs pro Gewebe



Assemblierung bei 0% Mismatch
mit GAP4 (Staden)



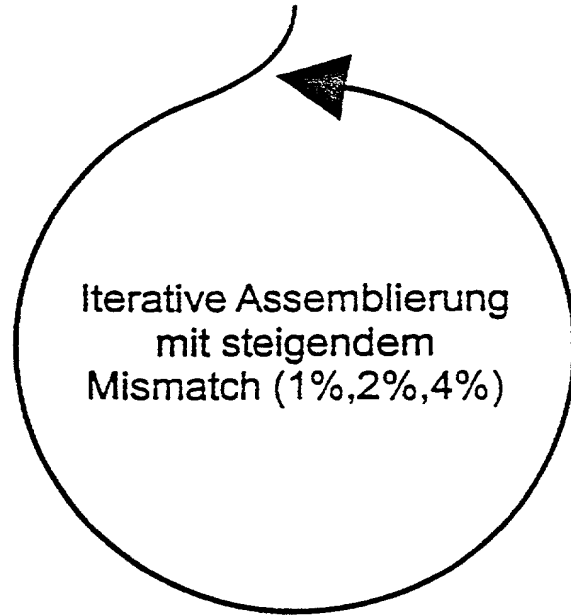
Contigs



Singletons



In Anzahl und Länge
zunehmende Contigs



5000-6000 Contigs ~25.000 übrige Singletons



~30.000 Konsensus-
sequenzen pro Gewebe

Fig. 2a

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-50,000 ESTs of a tissue (e.g.: uterus tumor)

GAP4 Assembly 1st Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 0

GAP4 Database 1
Contigs 1
Singletons 1

unassembled
ESTs

GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 1

GAP4 Database 2
Contigs 2
Singletons 2

unassembled
ESTs

GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2

GAP4 Database 3:
Contigs 3
Singletons 3

unassembled
ESTs

Figure 2b1

REPLACEMENT PAGE (RULE 26)

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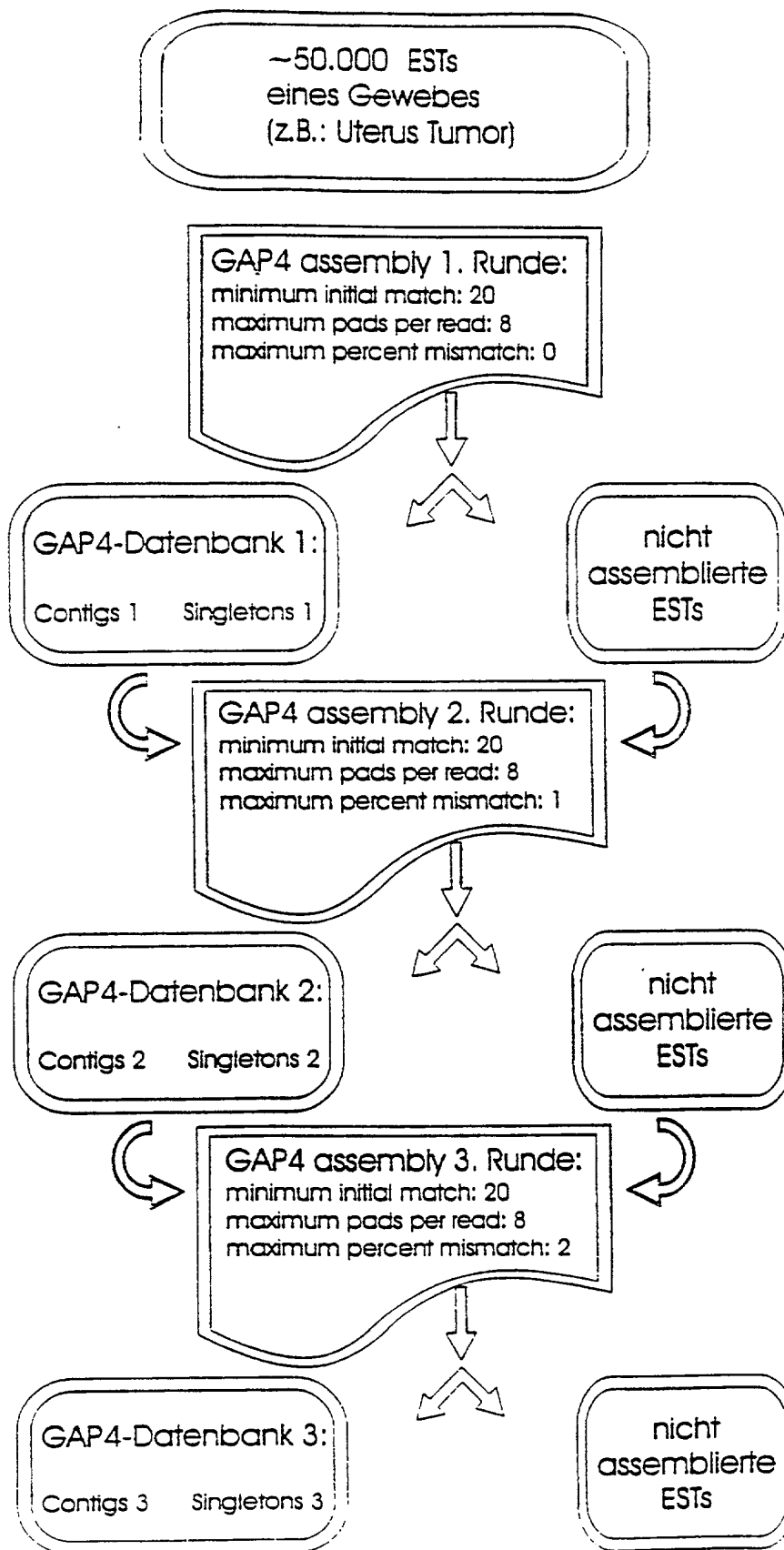


Fig. 2b1

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GAP4 Database 3:
Contigs 3
Singletons 3

unassembled
ESTs

Consensus 3

GAP4 Assembly 4th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2

GAP4 Database 4:
Contigs 4
Singletons 4

unassembled
ESTs

Consensus 4

GAP4 Assembly 5th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

GAP4 Database 5:
Contigs 5
Singletons 5

unassembled
ESTs 5

Consensus 5

Singletons 5

Figure 2b2

REPLACEMENT PAGE (RULE 26)

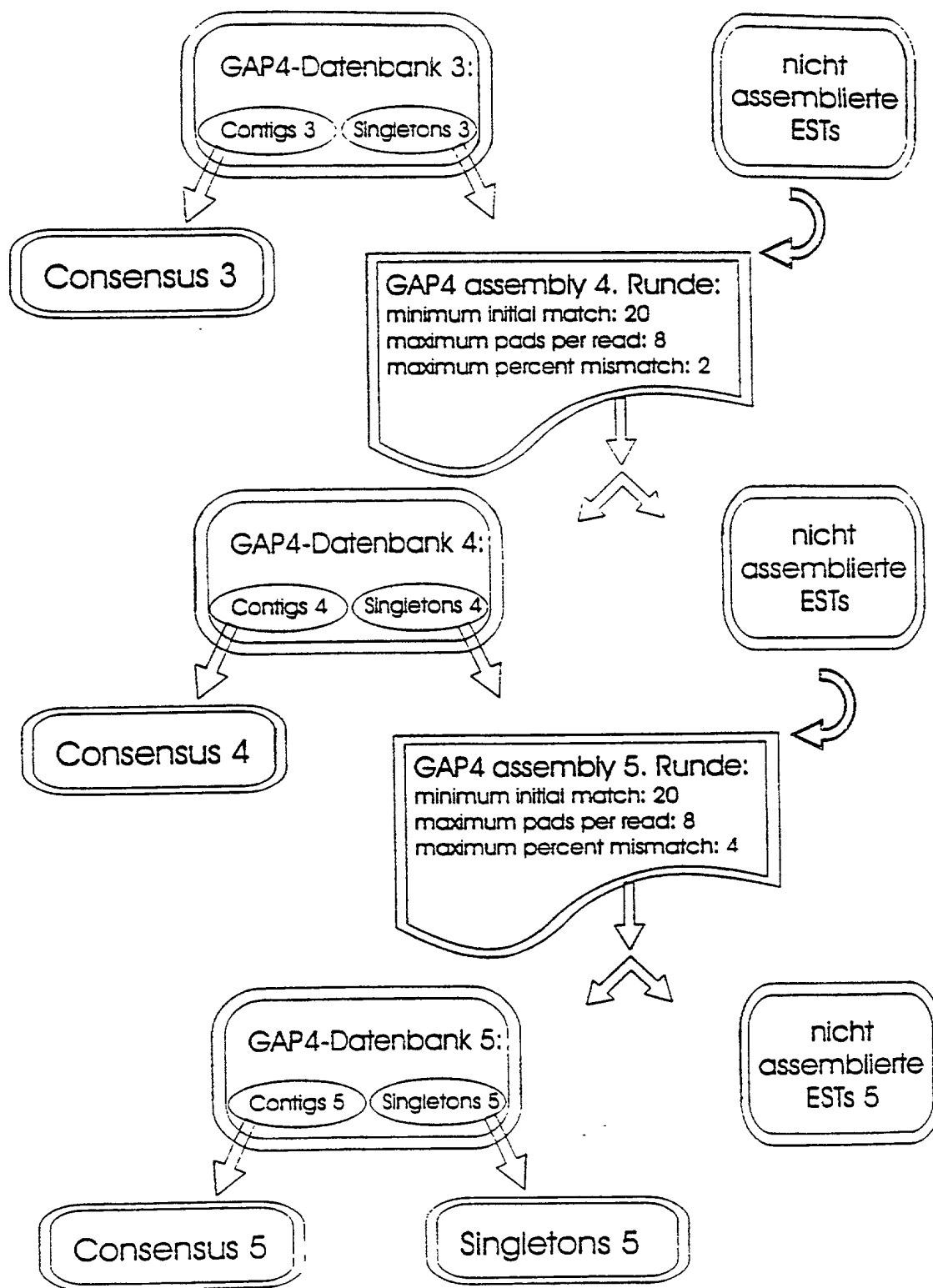


Fig. 2b2

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Consensus 3 Singletons 5

Consensus 4 unassembled
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

Assembled database
of a specific tissue
(e.g.: uterus tumor)

Figure 2b3

REPLACEMENT PAGE (RULE 26)

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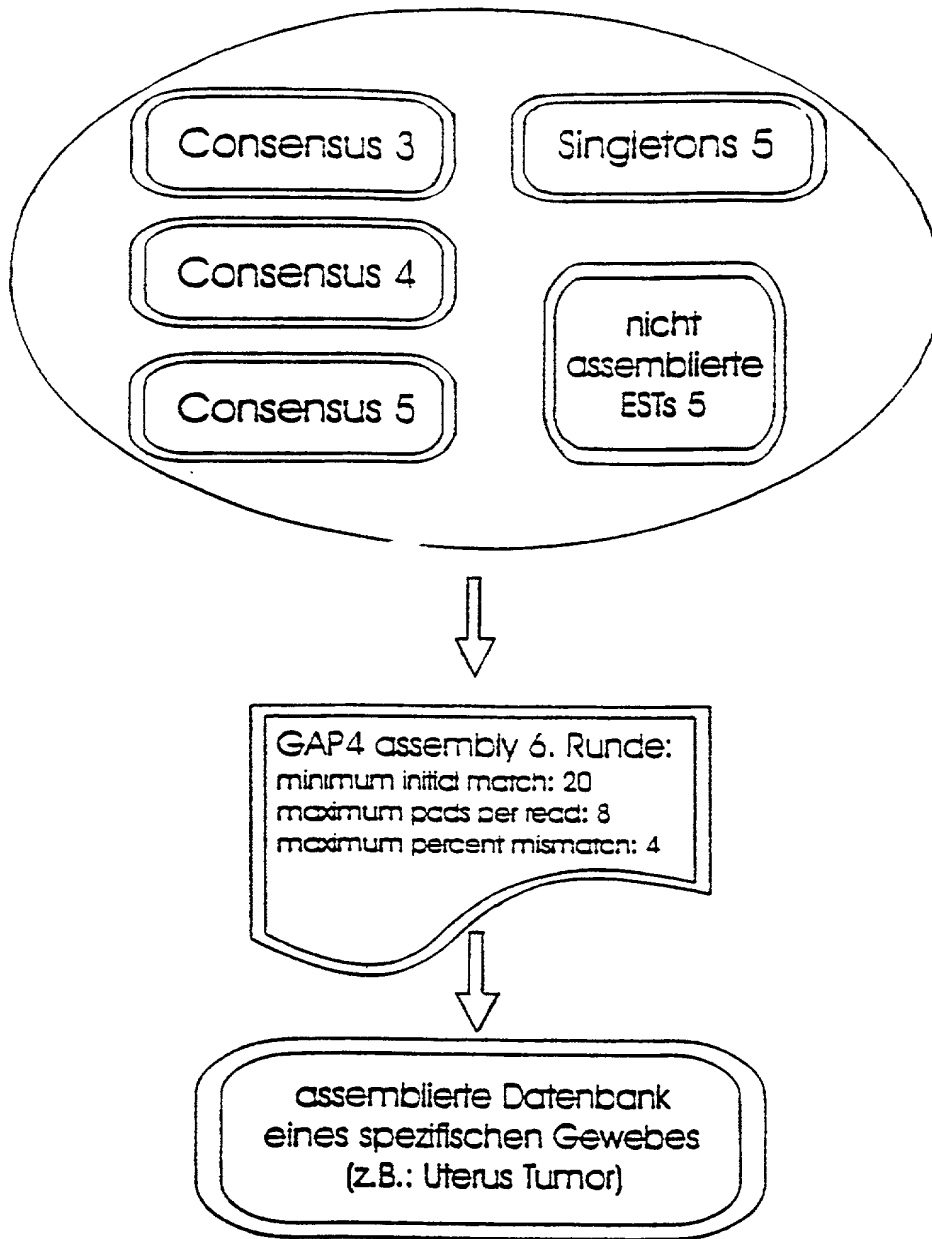


Fig. 2b3

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Assembled database
of a specific tissue
(e.g.: uterus tumor)

Consensus 6

Read-in as singletons

Database
of a specific tissue
(e.g.: uterus tumor)

Database of a second
specific tissue
(e.g.: normal uterus)

GAP4 Assembly
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 4

Tumor tissue-
specific ESTs

Non-tissue-
specific ESTs

Normal tissue-
specific ESTs

Fig. 2b4

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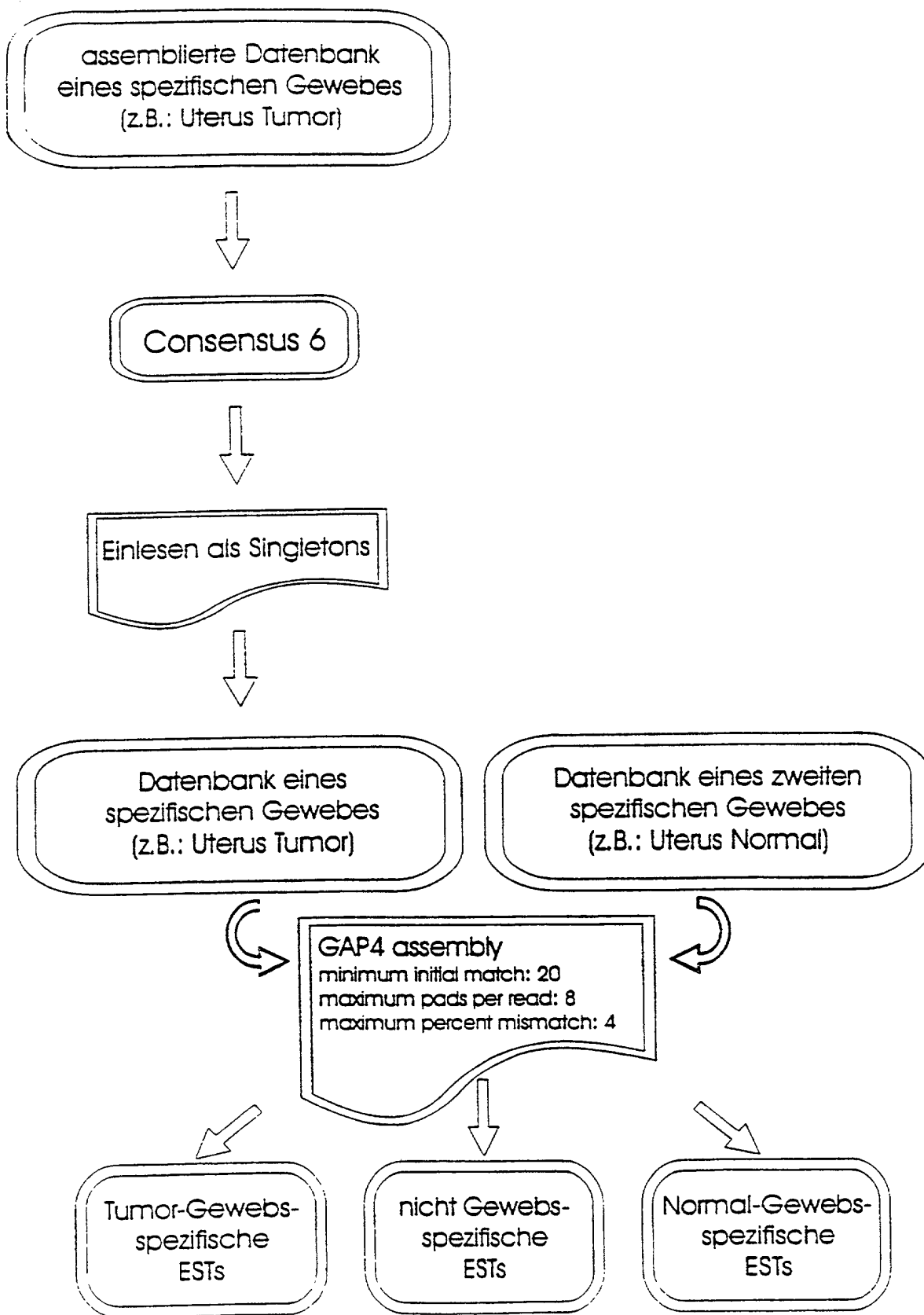


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
tumor tissue

Assembling at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

Figure 3

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In silico Subtraktion der Genexpression in verschiedenen Geweben

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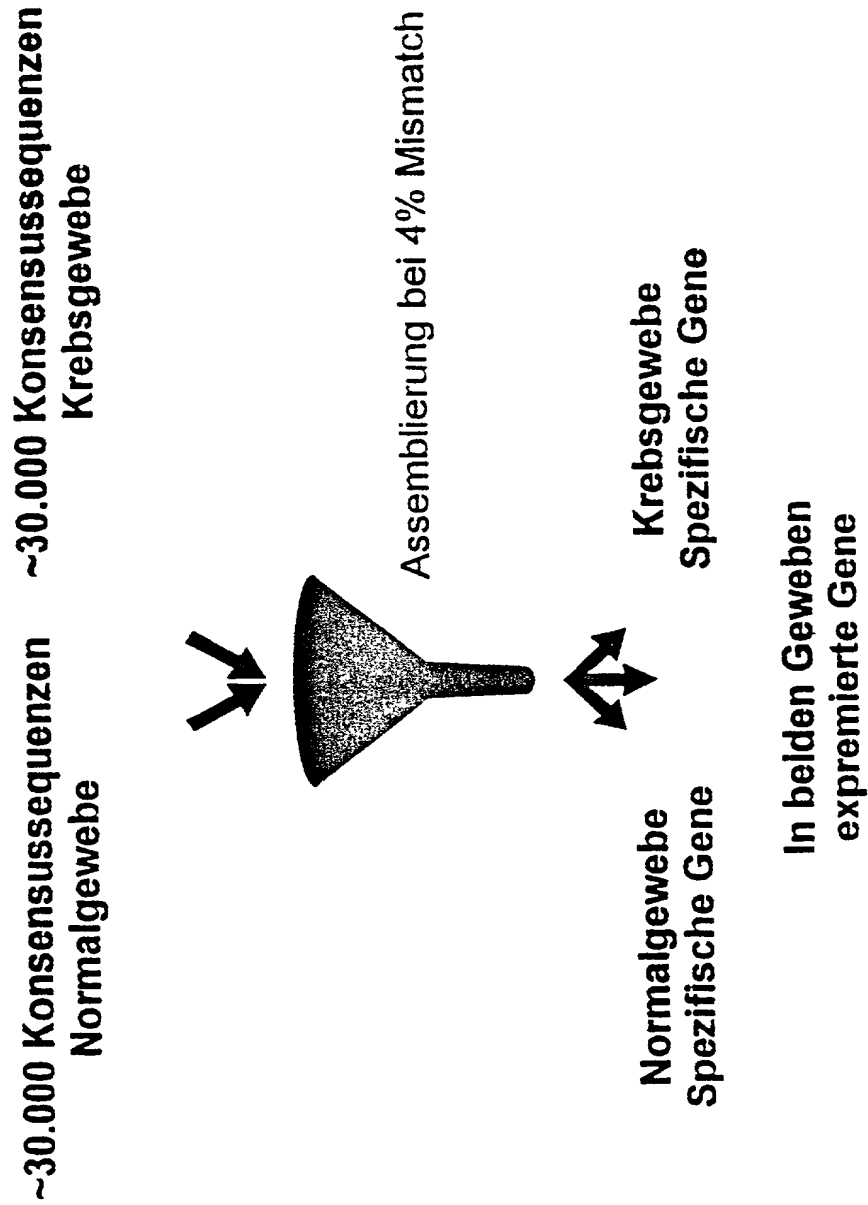


Fig. 3

Genes of interest

Determination of tissue-specific expression
via electronic Northern (INCYTE LifeSeq and
public EST databases)

Candidate genes for tumor suppressors or
tumor activators

Figure 4a

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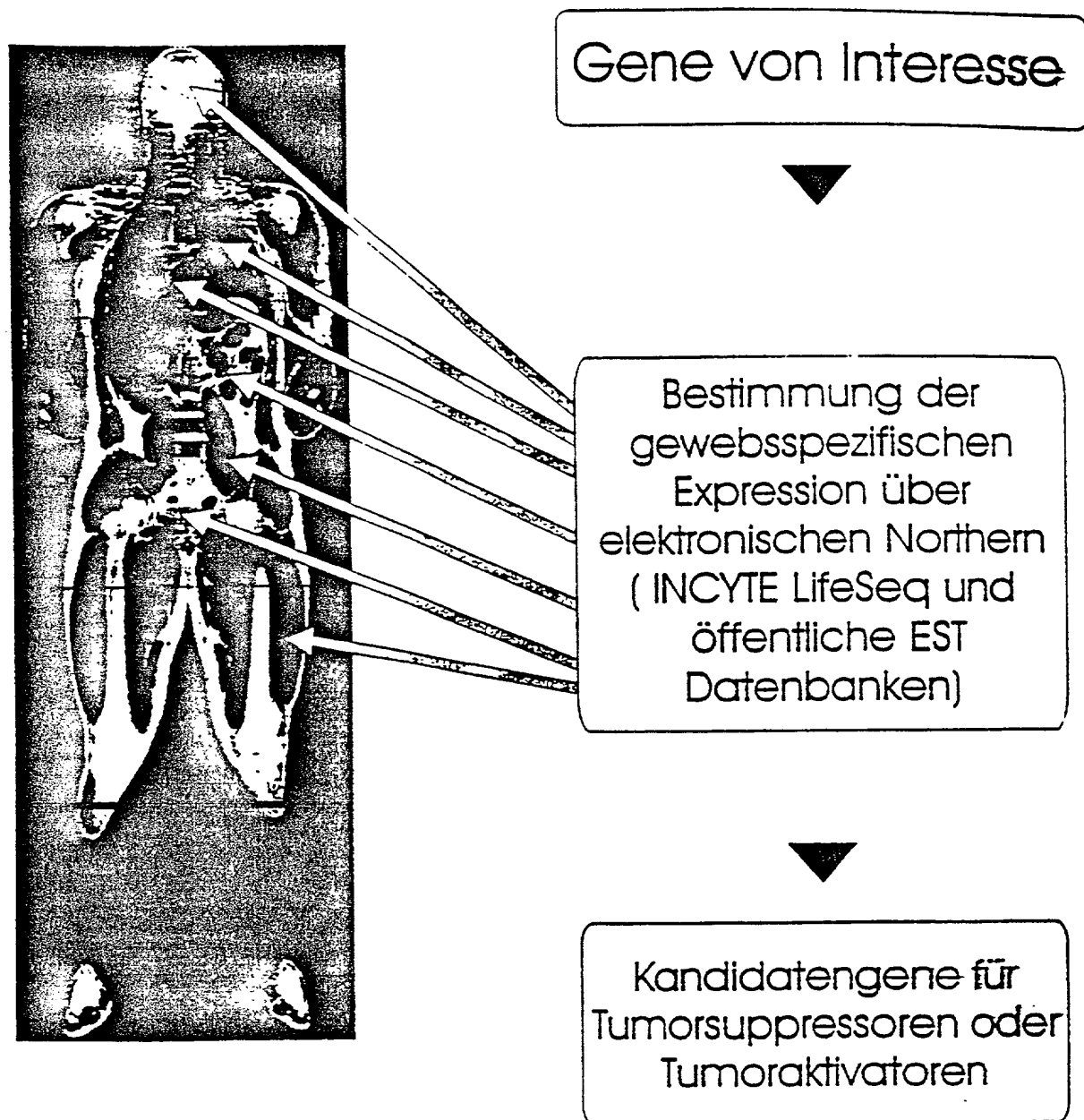


Fig. 4a

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Partial cDNA sequence
e.g. EST or contig
S

...GCCTCAAGTTATC...

WHILE $C_i > C_{i-1}$

Electronic Northern Blot

Fisher's Exact Test IF H_0 EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

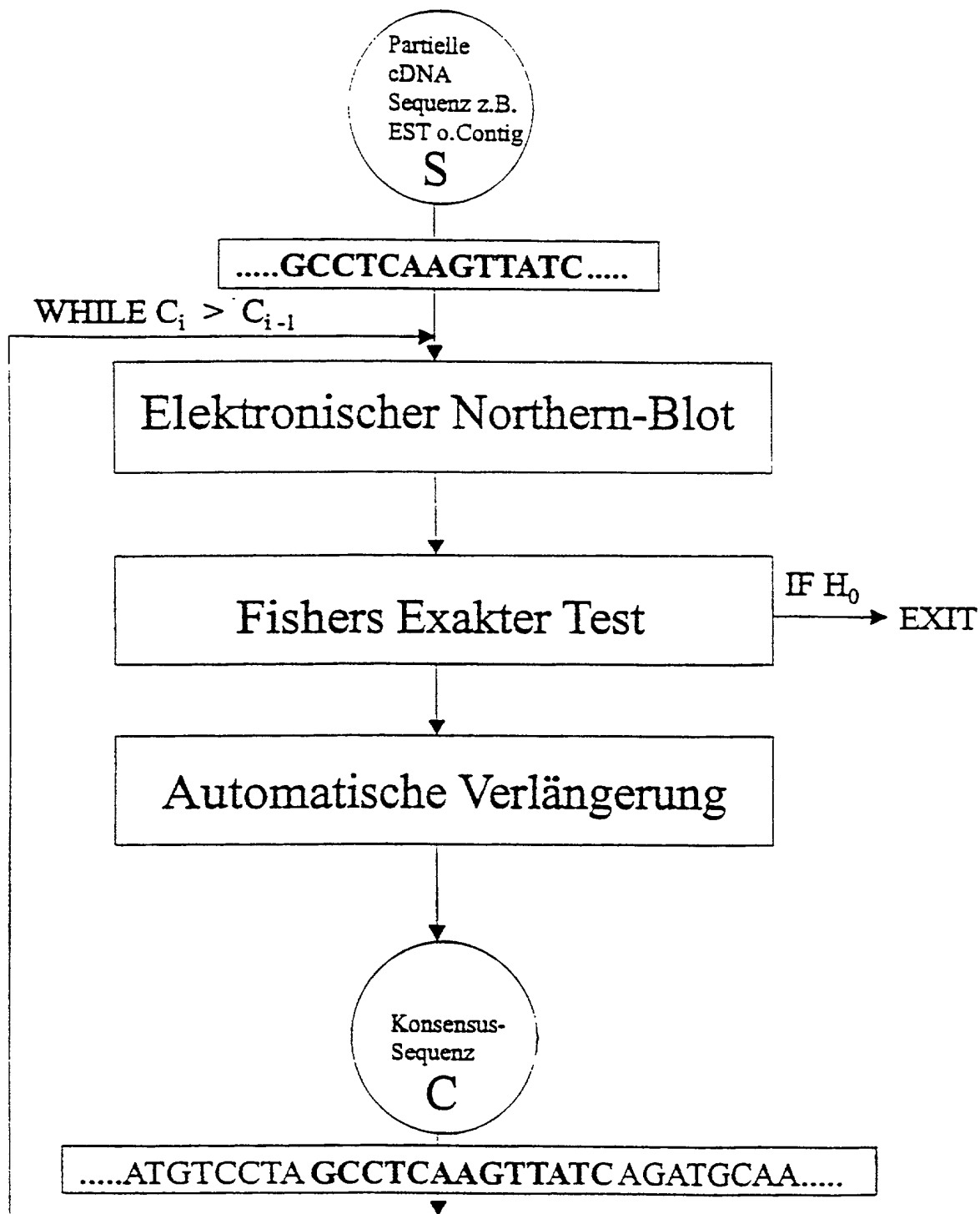


Fig. 4b

Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

REPLACEMENT PAGE (RULE 26)

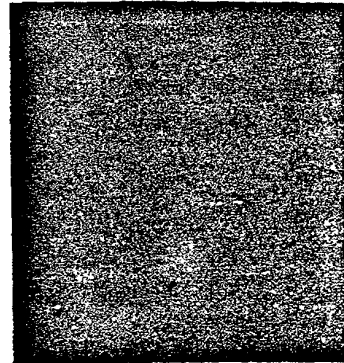
Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5

Systematic Gene Search in the Incyte LifeSeq Database

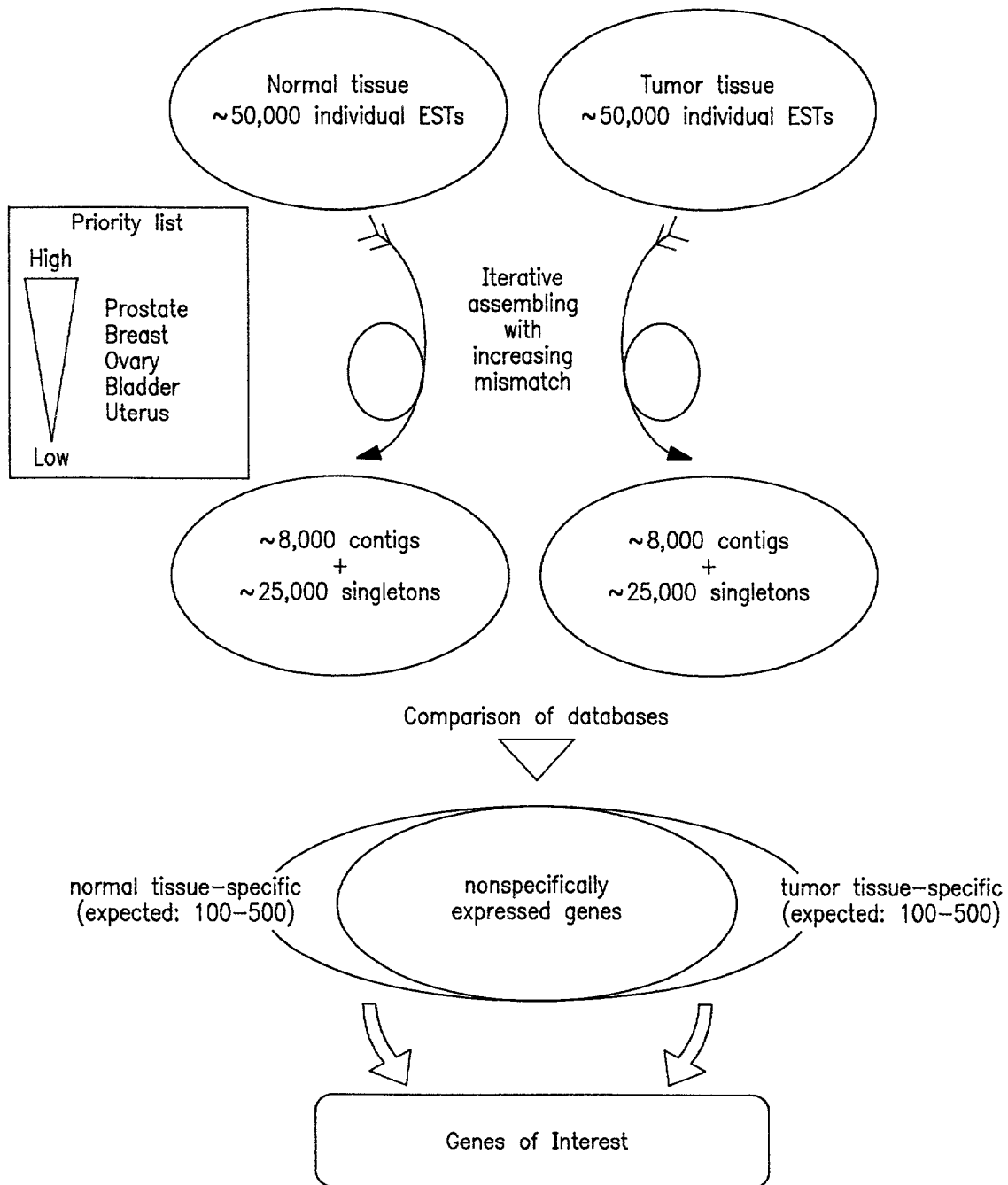


FIG. 1

Principle of EST Assembly

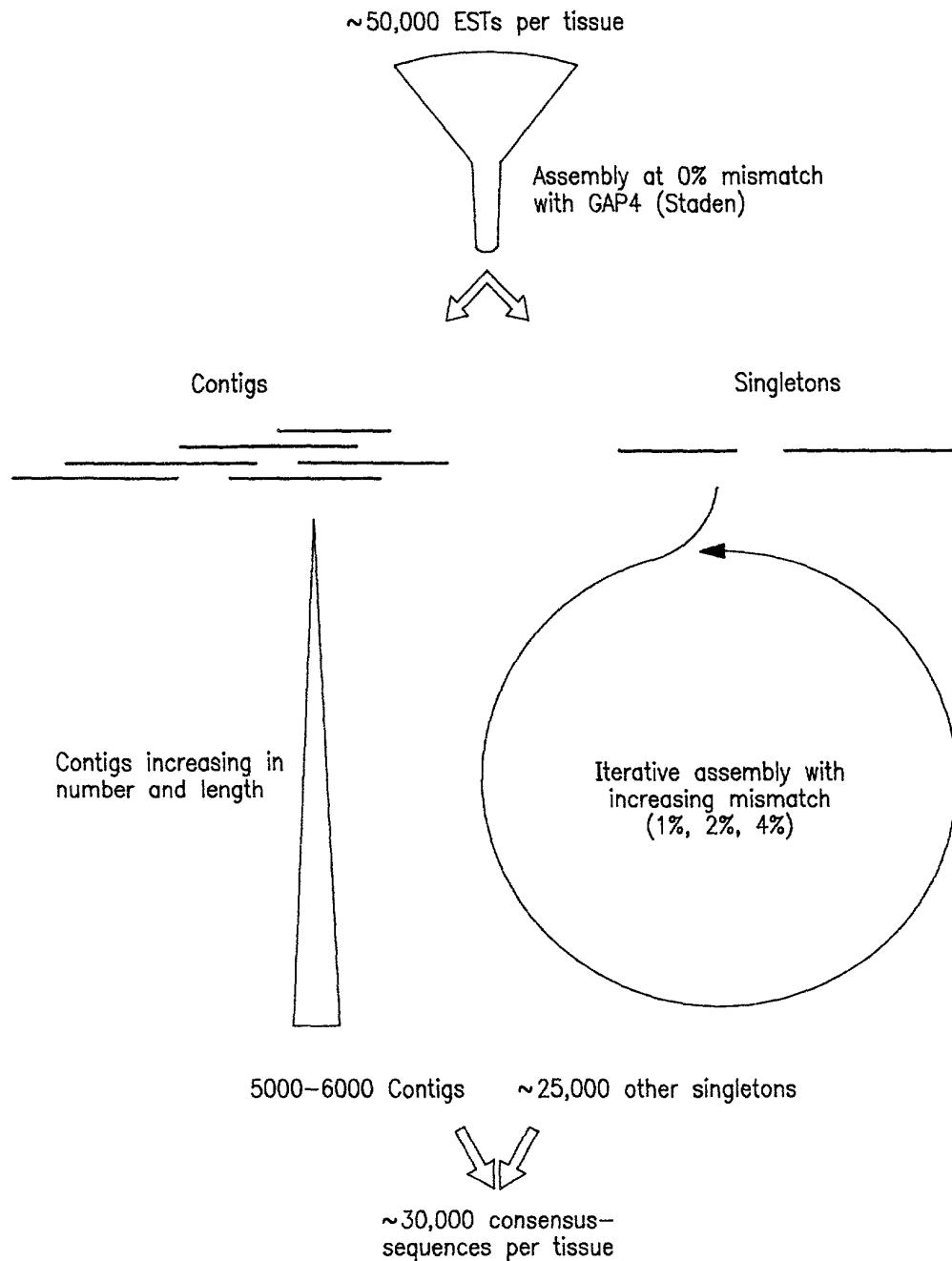


FIG. 2a

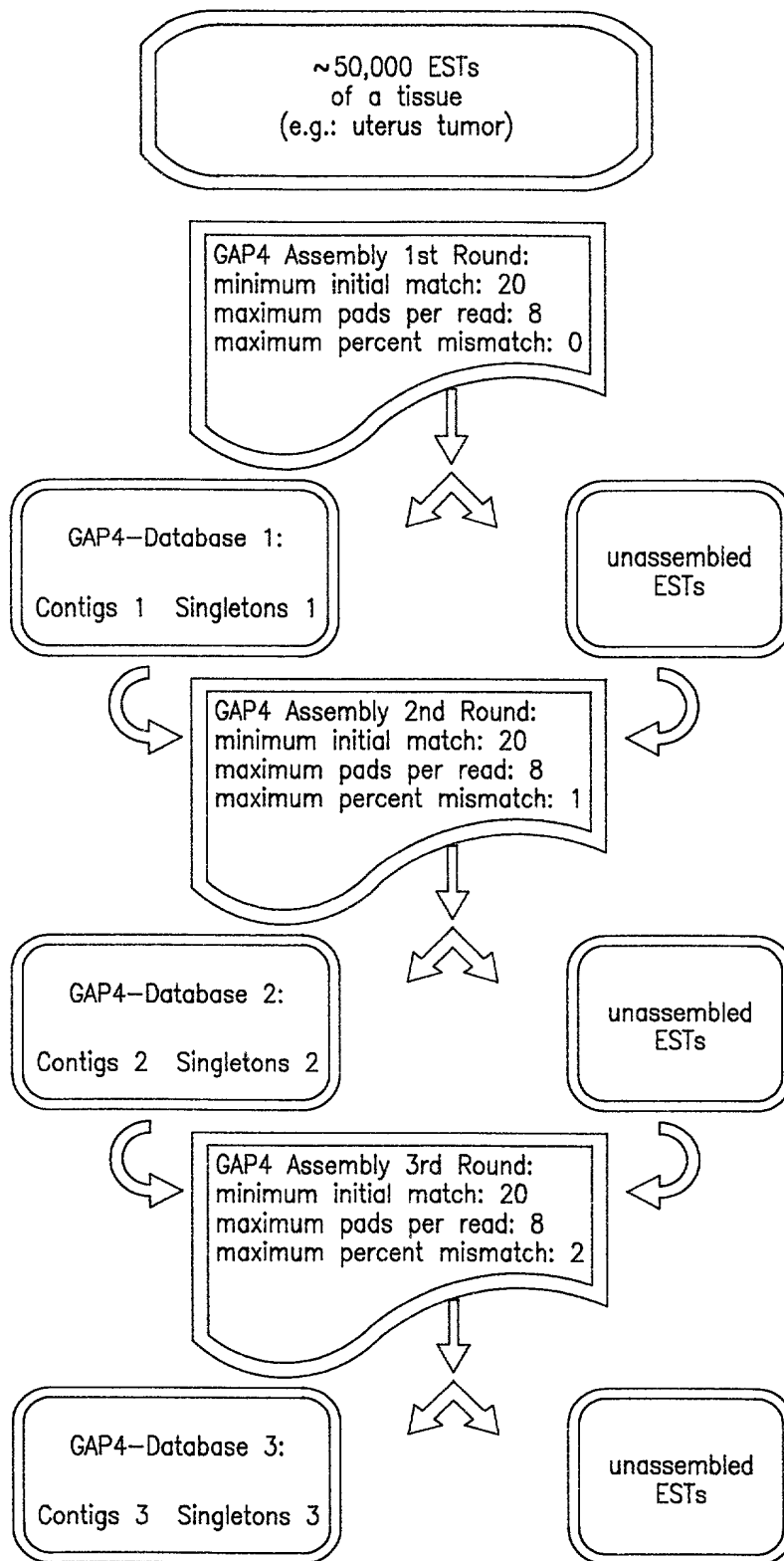


FIG. 2b-1

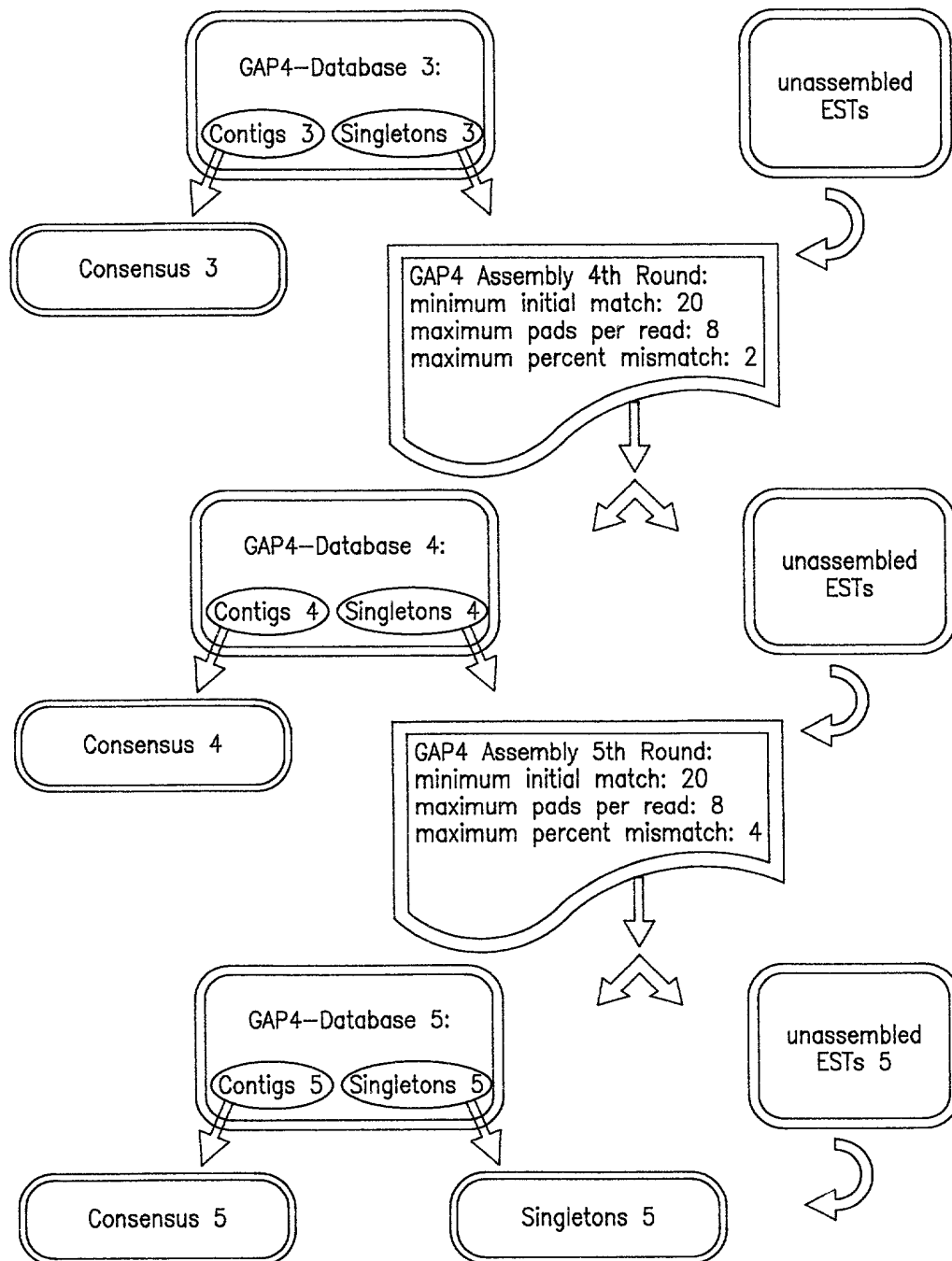


FIG. 2b-2

09/623746

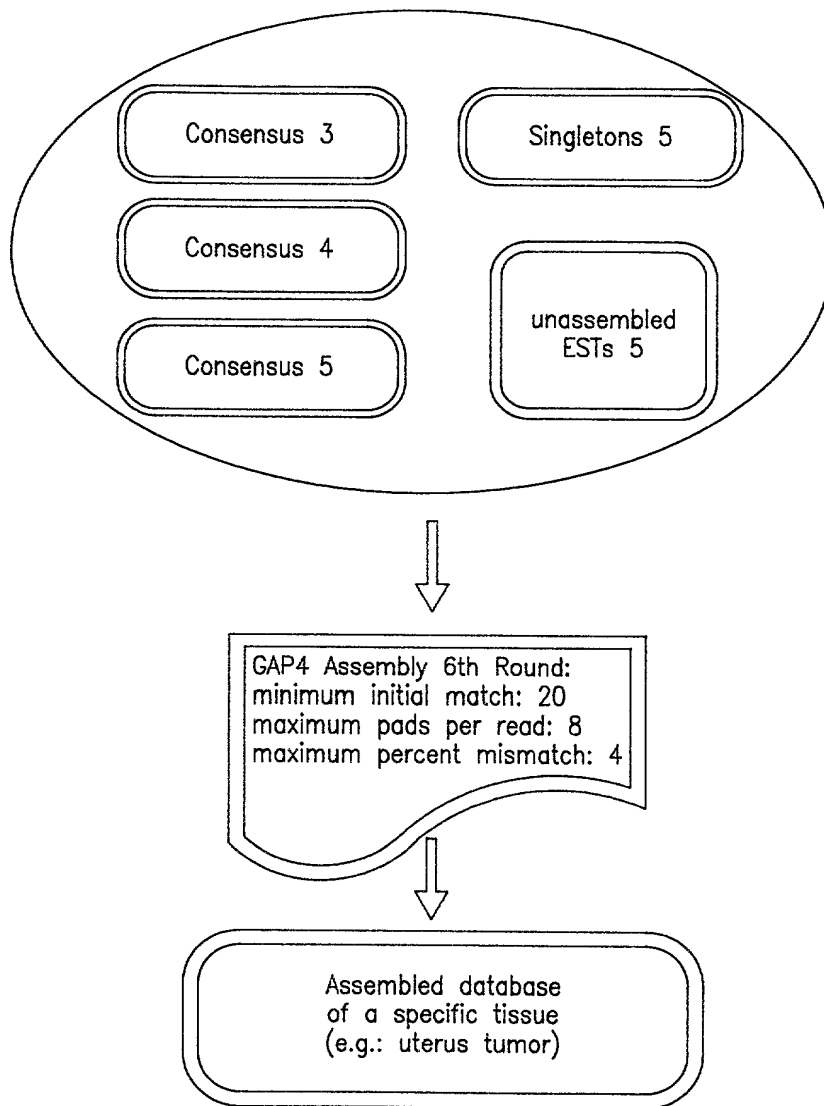


FIG. 2b-3

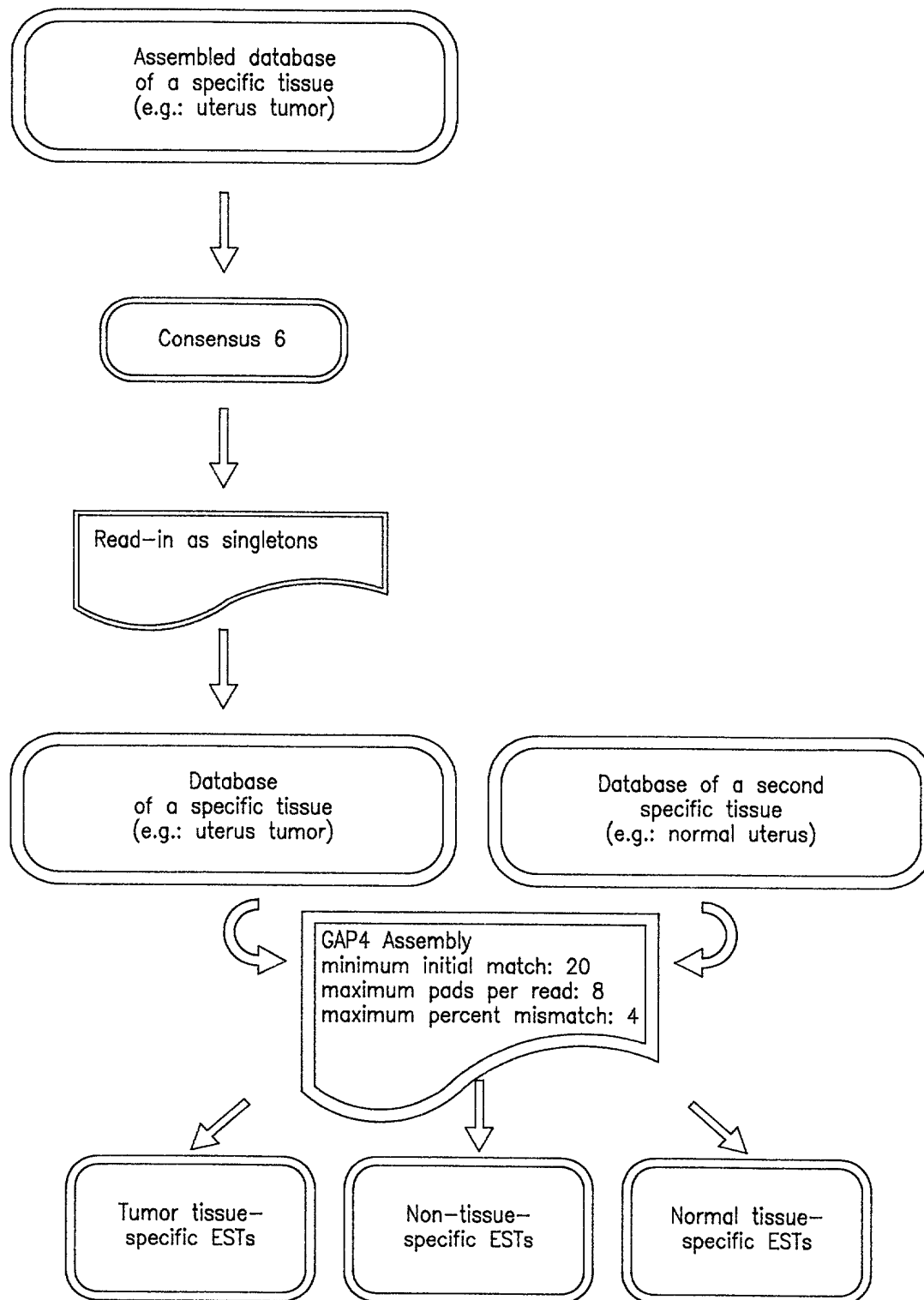


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue

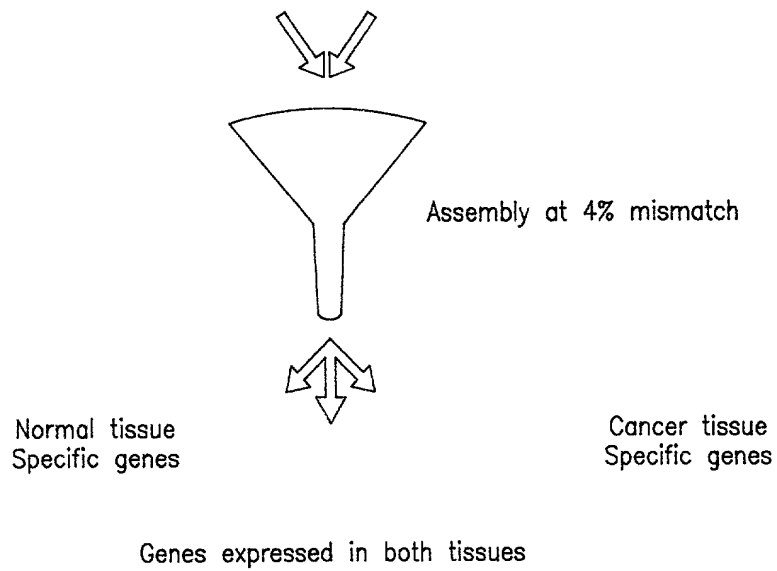


FIG. 3

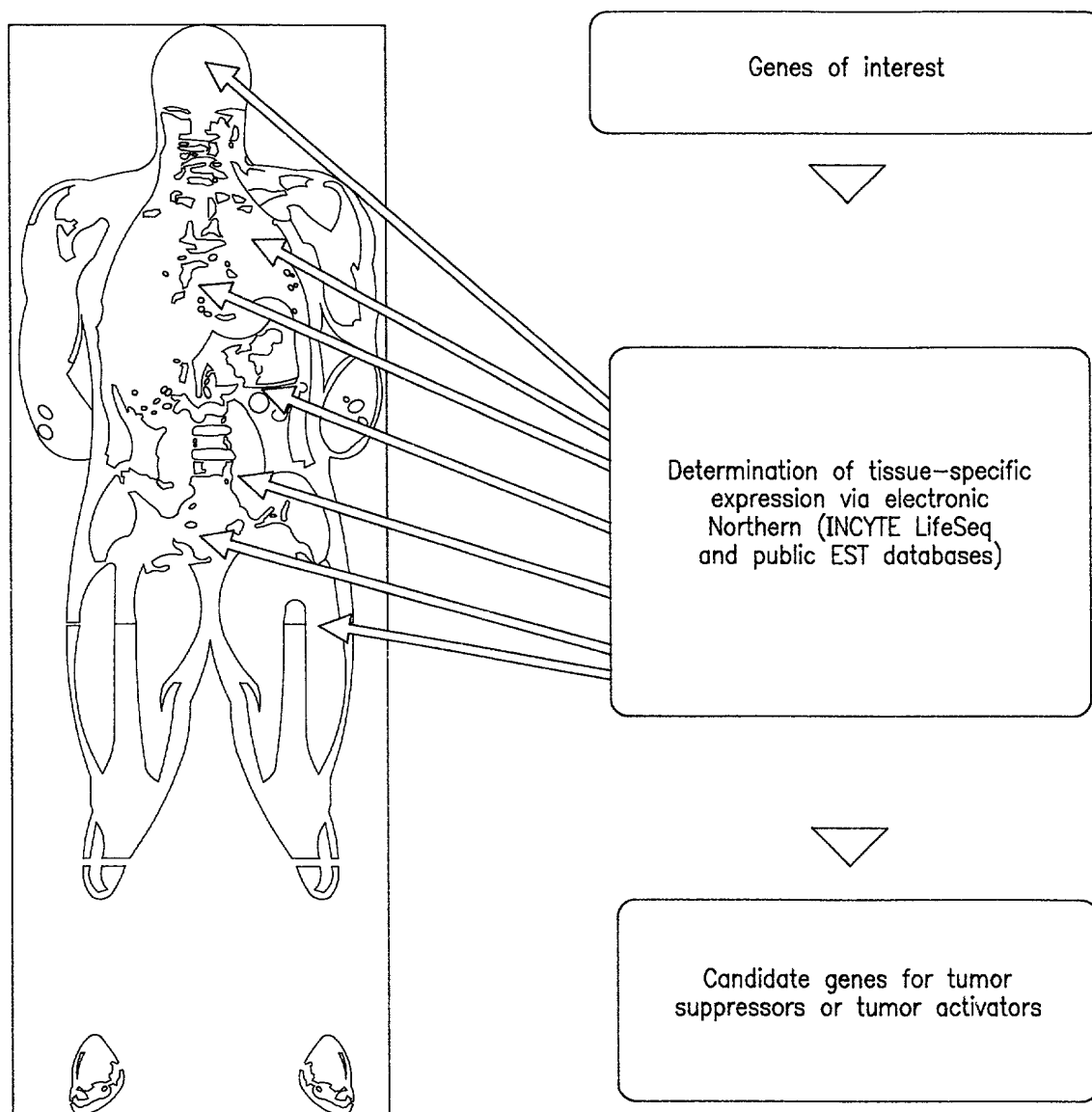


FIG. 4a

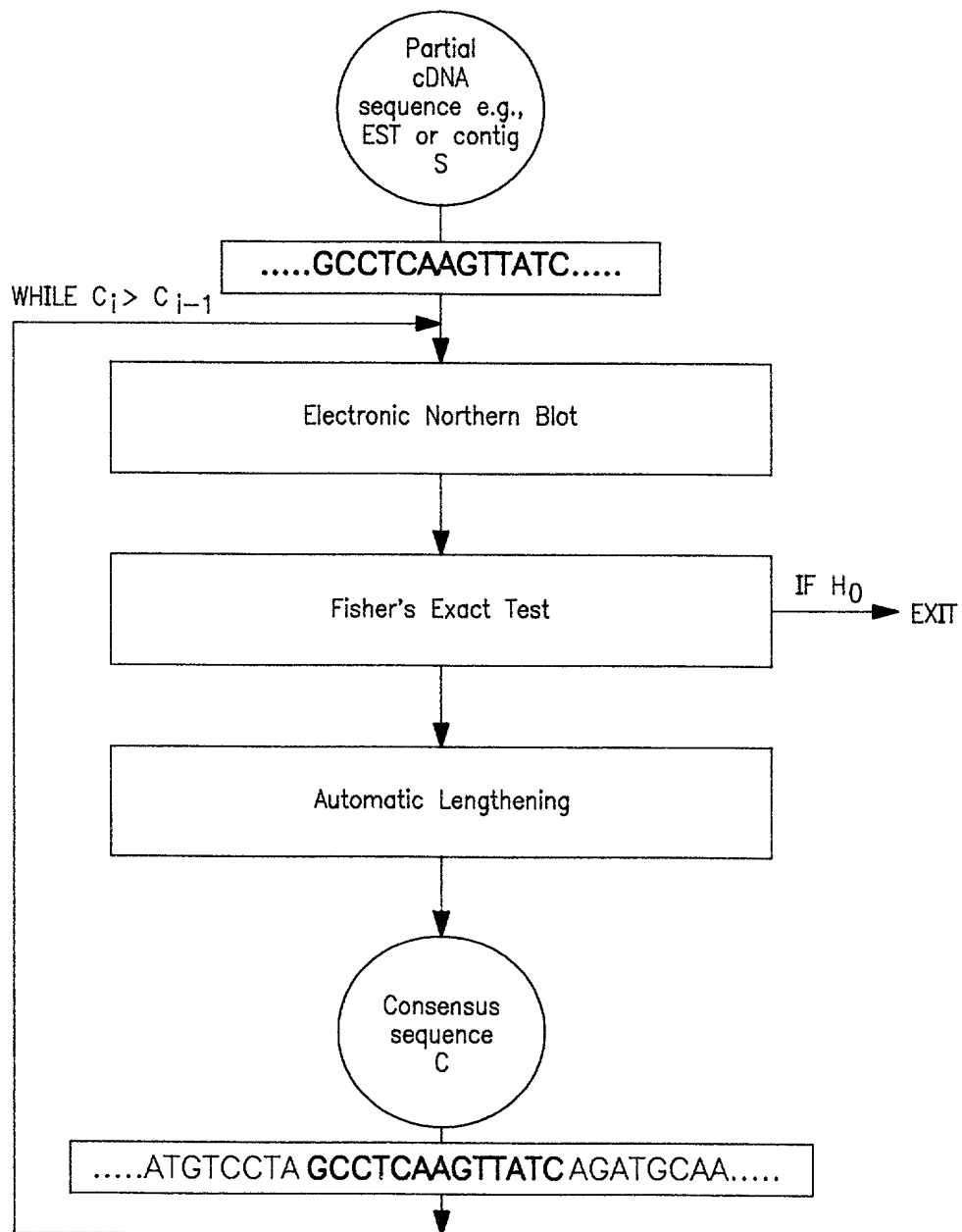


FIG. 4b

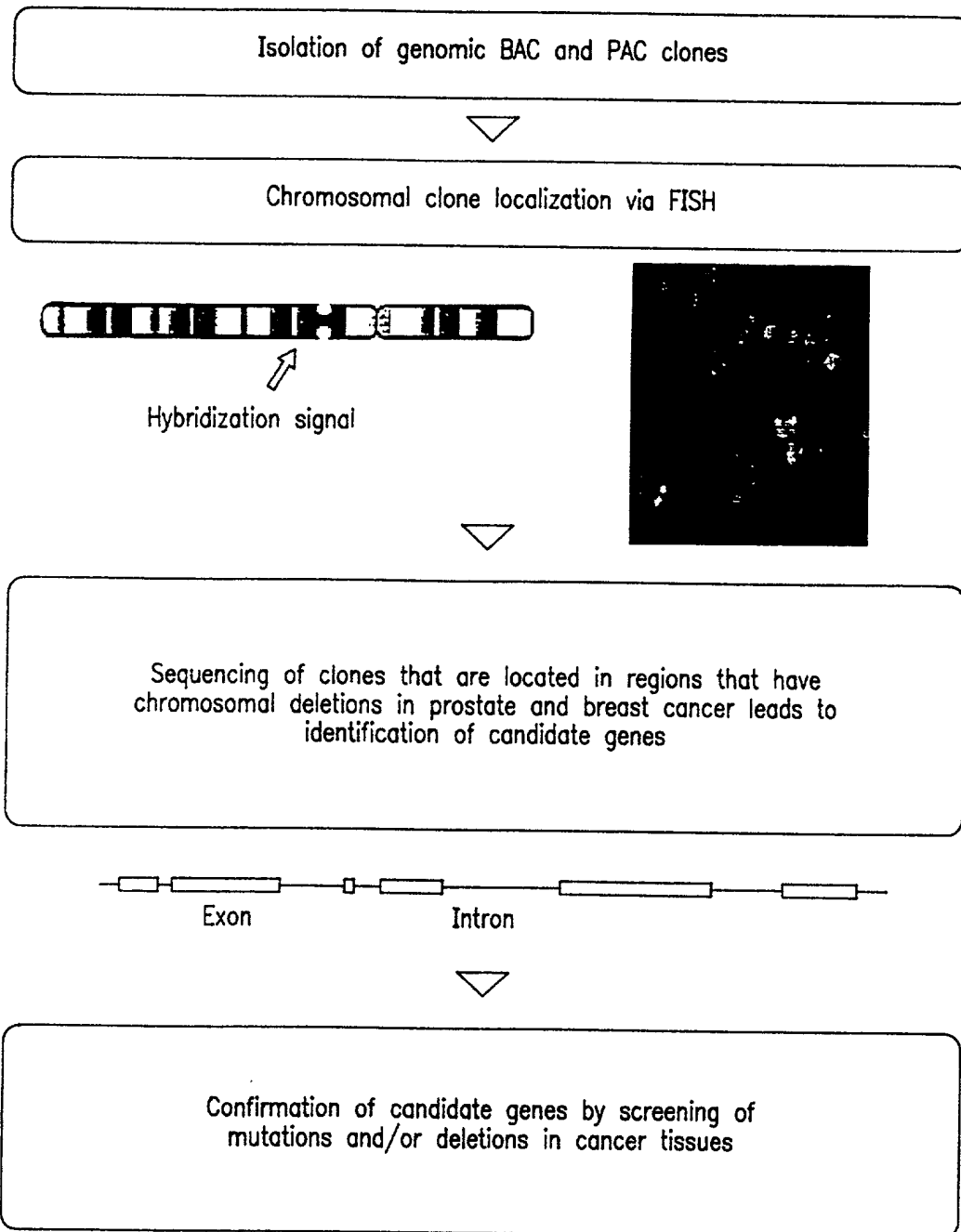


FIG. 5

Attorney Docket Number SCH 1761**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

HUMAN NUCLEIC ACID SEQUENCES FROM PROSTATE TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 9 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00722 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 11 194.0	GERMANY	10/03/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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15

Declaration for Patent Application (Continued)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

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☐ Additional joint inventors are named on separately numbered sheets attached hereto.

K:\PAT\Scn1763\Decl wpd

Attorney Docket Number SCH 1761

DECLARATION FOR PATENT APPLICATION

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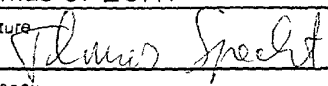
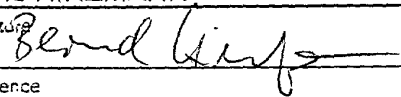
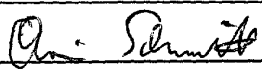
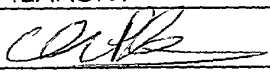
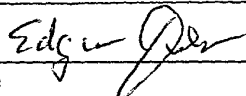
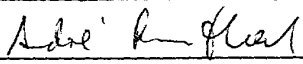
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Bernd HINZMANN	
Signature 	Date 29/08/00
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Armin SCHMITT	
Signature 	Date September 4, 2000
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Christian PILARSKY	
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Post Office Address Heinrich-Lange-Strasse 13c D-01474 Schönfeld, Germany	
Full Name of additional joint inventor (given name, family name)	
Edgar DAHL	
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Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany	
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André ROSENTHAL	
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Post Office Address Koppenplatz 10 D-10115 Berlin, Germany	

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